# SCORE Search Results Details for Application 10821669 and Search Result us-10-821-669-1_copy_673_691.szlm30.rapbn.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10821669 and Search Result us-10-821-669-1_copy_673_691.szlm30.rapbn.

start

Go Back to previous

Search Report

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                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:         November  1, 2006, 13:47:00 ; Search time 10.5556 Seconds
                                            (without alignments)
                                            150.742 Million cell updates/sec

Title:          US-10-821-669-1_COPY_673_691
Perfect score:  91
Sequence:       1 IPVLGTFALVSYIANKVLT 19

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       320231 seqs, 83745634 residues

Total number of hits satisfying chosen parameters:      64061

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :        Published_Applications_AA_New:*
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                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES

                  %
Result          Query
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RESULT 3
US-11-134-871-3348
; Sequence 3348, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
;  APPLICANT: Aebersold, Rudolf H.
;  APPLICANT:  Zhang, Hui
;  TITLE OF INVENTION: Compositions and Methods for
;  TITLE OF INVENTION:  Quatification of Serum Glycoproteins
;  FILE REFERENCE: 66661-116
;  CURRENT APPLICATION NUMBER: US/11/134,871
;  CURRENT FILING DATE:  2005-05-20
;  PRIOR APPLICATION NUMBER: 60/573,593
;  PRIOR FILING DATE: 2004-05-21
;  NUMBER OF SEQ ID NOS: 3602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3348
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-134-871-3348

  Query Match             33.0%;  Score 30;  DB 7;  Length 19;
  Best Local Similarity   85.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FALVSYI 13
              ||||:||
Db          9 FALVNYI 15
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673-691

RESULT 8
US-11-254-500-25
; Sequence 25, Application US/11254500
; Publication No. US20060147442A1
; GENERAL INFORMATION:
; APPLICANT: Homan, Jane
; APPLICANT: Imboden, Michael D.
; APPLICANT: Riggs, Michael D.
; APPLICANT: Carryn, Stephane D.
; TITLE OF INVENTION: Biocides
; FILE REFERENCE: IOGEN-10173
; CURRENT APPLICATION NUMBER: US/11/254,500
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Apis mellifera
US-11-254-500-25

673-691

Query Match 30.8%; Score 28; DB 7; Length 27;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db         12 GLPALISWISRK 23
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RESULT 4
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ID   Q57012_STAAU   PRELIMINARY;   PRT;    19 AA.
AC   Q57012;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Peptide L.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86135972; PubMed=3004956;
RA   Murphy E., Huwyler L., Do Carno de Freire Bastos M.;
RT   "Transposon Tn554: complete nucleotide sequence and isolation of
RT   transposition-defective and antibiotic-sensitive mutants.";
RL   EMBO J. 4:3357-3365(1985).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X03216; CAA26965.1; -; Genomic_DNA.
DR   InterPro; IPR013204; Leader_Erm.
SQ   SEQUENCE   19 AA;  2257 MW;  19F81AD99E4F2F9B CRC64;

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Qy          4 LGTFALVSYIANKV 17
              :|||::  :: |||
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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

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Perfect score: 98
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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4: geneseqp2001s:*
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6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 98 | 100.0 | 27 | 9 | ADW11113 | Adw11113 Clostridi |
| 3 | 52 | 53.1 | 12 | 9 | ADY20753 | Ady20753 Botulinum |
| 4 | 43 | 43.9 | 9 | 9 | ADZ69803 | Adz69803 Botulinum |
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| 7 | 38.5 | 39.3 | 22 | 2 | AAY19349 | Aay19349 Lecithin: |
| 8 | 38.5 | 39.3 | 22 | 2 | AAY18578 | Aay18578 Lecithin: |
| 9 | 38.5 | 39.3 | 22 | 8 | ADG21058 | Adg21058 Apolipopr |
| 10 | 38.5 | 39.3 | 22 | 8 | ADJ33000 | Adj33000 Apo lipop |
| 11 | 38 | 38.8 | 22 | 2 | AAY18741 | Aay18741 Lecithin: |
| 12 | 38 | 38.8 | 22 | 2 | AAY18995 | Aay18995 Lecithin: |

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| 13 | 38 | 38.8 | 22 | 2 | AAY19249 | Aay19249 Lecithin: |
| 14 | 38 | 38.8 | 22 | 2 | AAY18478 | Aay18478 Lecithin: |
| 15 | 38 | 38.8 | 22 | 8 | ADG20958 | Adg20958 Apolipopr |
| 16 | 38 | 38.8 | 22 | 8 | ADJ32900 | Adj32900 Apo lipop |
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| 18 | 36 | 36.7 | 22 | 9 | AEB28559 | Aeb28559 Human apo |
| 19 | 36 | 36.7 | 22 | 9 | AEB11518 | Aeb11518 Apolipopr |
| 20 | 35 | 35.7 | 9 | 9 | ADZ69802 | Adz69802 Botulinum |
| 21 | 35 | 35.7 | 14 | 9 | ADY81602 | Ady81602 HIV-1 ant |
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| 23 | 35 | 35.7 | 16 | 9 | ADY81604 | Ady81604 HIV-1 ant |
| 24 | 35 | 35.7 | 17 | 9 | ADY81605 | Ady81605 HIV-1 ant |
| 25 | 35 | 35.7 | 27 | 6 | ABP99874 | Abp99874 Breast sp |
| 26 | 35 | 35.7 | 27 | 8 | ADF85937 | Adf85937 Human bre |
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| 28 | 35 | 35.7 | 29 | 4 | AAM73708 | Aam73708 Human bon |
| 29 | 35 | 35.7 | 29 | 4 | AAM61013 | Aam61013 Human bra |
| 30 | 35 | 35.7 | 29 | 4 | ABG55445 | Abg55445 Human liv |
| 31 | 35 | 35.7 | 29 | 5 | ABG43583 | Abg43583 Human pep |
| 32 | 35 | 35.7 | 30 | 5 | AAU79980 | Aau79980 Human mal |
| 33 | 34.5 | 35.2 | 27 | 5 | AAE17354 | Aae17354 Bovine vi |
| 34 | 34.5 | 35.2 | 27 | 5 | AAE17325 | Aae17325 Recombina |
| 35 | 34.5 | 35.2 | 27 | 5 | AAE17327 | Aae17327 Recombina |
| 36 | 34.5 | 35.2 | 27 | 5 | AAE17356 | Aae17356 Border di |
| 37 | 34.5 | 35.2 | 27 | 5 | AAE17355 | Aae17355 Bovine vi |
| 38 | 34.5 | 35.2 | 27 | 5 | AAE17326 | Aae17326 Recombina |
| 39 | 34 | 34.7 | 29 | 3 | AAB23779 | Aab23779 Entry vec |
| 40 | 33.5 | 34.2 | 22 | 2 | AAY18850 | Aay18850 Lecithin: |
| 41 | 33.5 | 34.2 | 22 | 2 | AAY19104 | Aay19104 Lecithin: |
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| 43 | 33.5 | 34.2 | 22 | 2 | AAY18587 | Aay18587 Lecithin: |
| 44 | 33.5 | 34.2 | 22 | 8 | ADG21067 | Adg21067 Apolipopr |
| 45 | 33.5 | 34.2 | 22 | 8 | ADJ33009 | Adj33009 Apo lipop |
| 46 | 33 | 33.7 | 9 | 8 | ADK10588 | Adk10588 Human pap |
| 47 | 33 | 33.7 | 12 | 6 | ABP68020 | Abp68020 Bacillus |
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| 49 | 33 | 33.7 | 20 | 7 | ADD36371 | Add36371 Human THA |
| 50 | 33 | 33.7 | 20 | 8 | ADQ08994 | Adq08994 Human THA |
| 51 | 33 | 33.7 | 20 | 9 | ADW46173 | Adw46173 Human THA |
| 52 | 33 | 33.7 | 22 | 2 | AAY18785 | Aay18785 Lecithin: |
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| 54 | 33 | 33.7 | 22 | 2 | AAY18754 | Aay18754 Lecithin: |
| 55 | 33 | 33.7 | 22 | 2 | AAY19008 | Aay19008 Lecithin: |
| 56 | 33 | 33.7 | 22 | 2 | AAY19053 | Aay19053 Lecithin: |
| 57 | 33 | 33.7 | 22 | 2 | AAY19039 | Aay19039 Lecithin: |
| 58 | 33 | 33.7 | 22 | 2 | AAY19262 | Aay19262 Lecithin: |
| 59 | 33 | 33.7 | 22 | 2 | AAY19293 | Aay19293 Lecithin: |
| 60 | 33 | 33.7 | 22 | 2 | AAY19307 | Aay19307 Lecithin: |
| 61 | 33 | 33.7 | 22 | 2 | AAY18536 | Aay18536 Lecithin: |
| 62 | 33 | 33.7 | 22 | 2 | AAY18522 | Aay18522 Lecithin: |
| 63 | 33 | 33.7 | 22 | 2 | AAY18491 | Aay18491 Lecithin: |
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| 65 | 33 | 33.7 | 22 | 8 | ADG21016 | Adg21016 Apolipopr |
| 66 | 33 | 33.7 | 22 | 8 | ADG21002 | Adg21002 Apolipopr |
| 67 | 33 | 33.7 | 22 | 8 | ADJ32913 | Adj32913 Apo lipop |
| 68 | 33 | 33.7 | 22 | 8 | ADJ32944 | Adj32944 Apo lipop |
| 69 | 33 | 33.7 | 22 | 8 | ADJ32958 | Adj32958 Apo lipop |
| 70 | 33 | 33.7 | 26 | 5 | ABG66813 | Abg66813 Human pro |
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| 73 | 32 | 32.7 | 14 | 2 | AAW54723 | Aaw54723 Peptide f |

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| 74 | 32 | 32.7 | 14 | 7 | ADW33762 | Adw33762 HLA bindi |
| 75 | 32 | 32.7 | 14 | 7 | ADW34995 | Adw34995 HLA bindi |
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| 77 | 32 | 32.7 | 21 | 5 | AAU89228 | Aau89228 Insulin/i |
| 78 | 32 | 32.7 | 21 | 6 | ADA04050 | Ada04050 Insulin r |
| 79 | 32 | 32.7 | 21 | 7 | ADH95263 | Adh95263 Insulin r |
| 80 | 32 | 32.7 | 21 | 8 | ADL67954 | Adl67954 IGF-1R/IR |
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| 82 | 32 | 32.7 | 22 | 2 | AAY18788 | Aay18788 Lecithin: |
| 83 | 32 | 32.7 | 22 | 2 | AAY18801 | Aay18801 Lecithin: |
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| 86 | 32 | 32.7 | 22 | 2 | AAY19042 | Aay19042 Lecithin: |
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| 88 | 32 | 32.7 | 22 | 2 | AAY19055 | Aay19055 Lecithin: |
| 89 | 32 | 32.7 | 22 | 2 | AAY19098 | Aay19098 Lecithin: |
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| 93 | 32 | 32.7 | 22 | 2 | AAY19296 | Aay19296 Lecithin: |
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| 101 | 32 | 32.7 | 22 | 8 | ADG20960 | Adg20960 Apolipopr |
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| 103 | 32 | 32.7 | 22 | 8 | ADJ32947 | Adj32947 Apo lipop |
| 104 | 32 | 32.7 | 22 | 8 | ADJ33003 | Adj33003 Apo lipop |
| 105 | 32 | 32.7 | 22 | 8 | ADJ32960 | Adj32960 Apo lipop |
| 106 | 32 | 32.7 | 22 | 9 | AEB09648 | Aeb09648 Human apo |
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| 109 | 31.5 | 32.1 | 30 | 5 | ABP29138 | Abp29138 Streptoco |
| 110 | 31 | 31.6 | 8 | 9 | AEC13995 | Aec13995 Enterococ |
| 111 | 31 | 31.6 | 15 | 2 | AAW73756 | Aaw73756 M. tuberc |
| 112 | 31 | 31.6 | 15 | 2 | AAW73866 | Aaw73866 M. tuberc |
| 113 | 31 | 31.6 | 15 | 4 | AAU08222 | Aau08222 Mycobacte |
| 114 | 31 | 31.6 | 15 | 4 | AAB97804 | Aab97804 gp100 der |
| 115 | 31 | 31.6 | 15 | 4 | AAB98194 | Aab98194 Interfero |
| 116 | 31 | 31.6 | 21 | 6 | ABB82880 | Abb82880 Dopamine |
| 117 | 31 | 31.6 | 21 | 6 | ABP58824 | Abp58824 Melanoma- |
| 118 | 31 | 31.6 | 22 | 2 | AAW39966 | Aaw39966 Peptide e |
| 119 | 31 | 31.6 | 22 | 2 | AAY18720 | Aay18720 Lecithin: |
| 120 | 31 | 31.6 | 22 | 2 | AAY18810 | Aay18810 Lecithin: |
| 121 | 31 | 31.6 | 22 | 2 | AAY18852 | Aay18852 Lecithin: |
| 122 | 31 | 31.6 | 22 | 2 | AAY19106 | Aay19106 Lecithin: |
| 123 | 31 | 31.6 | 22 | 2 | AAY19064 | Aay19064 Lecithin: |
| 124 | 31 | 31.6 | 22 | 2 | AAY18974 | Aay18974 Lecithin: |
| 125 | 31 | 31.6 | 22 | 2 | AAY19318 | Aay19318 Lecithin: |
| 126 | 31 | 31.6 | 22 | 2 | AAY19228 | Aay19228 Lecithin: |
| 127 | 31 | 31.6 | 22 | 2 | AAY19360 | Aay19360 Lecithin: |
| 128 | 31 | 31.6 | 22 | 2 | AAY18457 | Aay18457 Lecithin: |
| 129 | 31 | 31.6 | 22 | 2 | AAY18547 | Aay18547 Lecithin: |
| 130 | 31 | 31.6 | 22 | 2 | AAY18589 | Aay18589 Lecithin: |
| 131 | 31 | 31.6 | 22 | 8 | ADG20937 | Adg20937 Apolipopr |
| 132 | 31 | 31.6 | 22 | 8 | ADG21027 | Adg21027 Apolipopr |
| 133 | 31 | 31.6 | 22 | 8 | ADG21069 | Adg21069 Apolipopr |
| 134 | 31 | 31.6 | 22 | 8 | ADJ33011 | Adj33011 Apo lipop |

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| 135 | 31 | 31.6 | 22 | 8 | ADJ32969 | Adj32969 Apo lipop |
| 136 | 31 | 31.6 | 22 | 8 | ADJ32879 | Adj32879 Apo lipop |
| 137 | 31 | 31.6 | 23 | 8 | ADM12473 | Adm12473 Ii-key/gp |
| 138 | 31 | 31.6 | 23 | 8 | ADO38696 | Ado38696 Melanocyt |
| 139 | 31 | 31.6 | 24 | 10 | AEF01181 | Aef01181 Ii-key/ g |
| 140 | 31 | 31.6 | 25 | 8 | ABO54473 | Abo54473 Human gen |
| 141 | 31 | 31.6 | 30 | 5 | AAU84859 | Aau84859 Human gp1 |
| 142 | 31 | 31.6 | 30 | 7 | ADG14992 | Adg14992 Human SEC |
| 143 | 30 | 30.6 | 10 | 5 | AAU82796 | Aau82796 Human Cal |
| 144 | 30 | 30.6 | 10 | 9 | ADW86252 | Adw86252 Human cal |
| 145 | 30 | 30.6 | 10 | 9 | ADZ88977 | Adz88977 Human cal |
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| 147 | 30 | 30.6 | 14 | 2 | AAR78128 | Aar78128 Bacterial |
| 148 | 30 | 30.6 | 14 | 2 | AAR82368 | Aar82368 BPI.264, |
| 149 | 30 | 30.6 | 14 | 2 | AAR87868 | Aar87868 BPI.264 f |
| 150 | 30 | 30.6 | 14 | 2 | AAR76447 | Aar76447 Bacterial |
| 151 | 30 | 30.6 | 14 | 2 | AAW06063 | Aaw06063 Recombina |
| 152 | 30 | 30.6 | 14 | 2 | AAW04138 | Aaw04138 Antifunga |
| 153 | 30 | 30.6 | 14 | 2 | AAW44503 | Aaw44503 Anti-fung |
| 154 | 30 | 30.6 | 14 | 2 | AAW43689 | Aaw43689 Bacterici |
| 155 | 30 | 30.6 | 14 | 2 | AAW63514 | Aaw63514 Human BPI |
| 156 | 30 | 30.6 | 14 | 2 | AAY00480 | Aay00480 Antifunga |
| 157 | 30 | 30.6 | 14 | 3 | AAB16254 | Aab16254 Bacterici |
| 158 | 30 | 30.6 | 14 | 4 | AAB65404 | Aab65404 Anti-fung |
| 159 | 30 | 30.6 | 14 | 4 | AAB52424 | Aab52424 Peptide B |
| 160 | 30 | 30.6 | 14 | 8 | ADI66714 | Adi66714 Rat bacte |
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| 162 | 30 | 30.6 | 15 | 2 | AAW73755 | Aaw73755 M. tuberc |
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| 164 | 30 | 30.6 | 15 | 4 | AAU08221 | Aau08221 Mycobacte |
| 165 | 30 | 30.6 | 15 | 4 | AAB86572 | Aab86572 Human cyt |
| 166 | 30 | 30.6 | 15 | 4 | AAB19894 | Aab19894 Neisseria |
| 167 | 30 | 30.6 | 15 | 8 | ADO77268 | Ado77268 Human 213 |
| 168 | 30 | 30.6 | 15 | 9 | ADW76239 | Adw76239 Human cyt |
| 169 | 30 | 30.6 | 15 | 9 | AEC14055 | Aec14055 Pseudomon |
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| 171 | 30 | 30.6 | 17 | 9 | AED44638 | Aed44638 Hs.516830 |
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| 173 | 30 | 30.6 | 18 | 4 | AAB77837 | Aab77837 Core poly |
| 174 | 30 | 30.6 | 18 | 10 | AEF02100 | Aef02100 Ii-key/ H |
| 175 | 30 | 30.6 | 19 | 2 | AAY18769 | Aay18769 Lecithin: |
| 176 | 30 | 30.6 | 19 | 2 | AAY19023 | Aay19023 Lecithin: |
| 177 | 30 | 30.6 | 19 | 2 | AAY19277 | Aay19277 Lecithin: |
| 178 | 30 | 30.6 | 19 | 2 | AAY18506 | Aay18506 Lecithin: |
| 179 | 30 | 30.6 | 19 | 7 | ADF14735 | Adf14735 Diabetes |
| 180 | 30 | 30.6 | 19 | 7 | ADF14736 | Adf14736 Diabetes |
| 181 | 30 | 30.6 | 19 | 8 | ADG20986 | Adg20986 Apolipopr |
| 182 | 30 | 30.6 | 19 | 8 | ADJ32928 | Adj32928 Apo lipop |
| 183 | 30 | 30.6 | 19 | 9 | ADW11059 | Adw11059 Clostridi |
| 184 | 30 | 30.6 | 20 | 2 | AAY18761 | Aay18761 Lecithin: |
| 185 | 30 | 30.6 | 20 | 2 | AAY19015 | Aay19015 Lecithin: |
| 186 | 30 | 30.6 | 20 | 2 | AAY19269 | Aay19269 Lecithin: |
| 187 | 30 | 30.6 | 20 | 2 | AAY18498 | Aay18498 Lecithin: |
| 188 | 30 | 30.6 | 20 | 3 | AAY89436 | Aay89436 Core poly |
| 189 | 30 | 30.6 | 20 | 3 | AAY96725 | Aay96725 MADr3 C-t |
| 190 | 30 | 30.6 | 20 | 4 | ABB02319 | Abb02319 Viral cor |
| 191 | 30 | 30.6 | 20 | 4 | ABB00844 | Abb00844 Viral DP1 |
| 192 | 30 | 30.6 | 20 | 4 | AAU13390 | Aau13390 DP178-lik |
| 193 | 30 | 30.6 | 20 | 5 | ADE02339 | Ade02339 Hybrid po |
| 194 | 30 | 30.6 | 20 | 8 | ADG20978 | Adg20978 Apolipopr |
| 195 | 30 | 30.6 | 20 | 8 | ADJ32920 | Adj32920 Apo lipop |

| | | | | | | |
|---|---|---|---|---|---|---|
| 196 | 30 | 30.6 | 21 | 2 | AAY18744 | Aay18744 Lecithin: |
| 197 | 30 | 30.6 | 21 | 2 | AAY18998 | Aay18998 Lecithin: |
| 198 | 30 | 30.6 | 21 | 2 | AAY19252 | Aay19252 Lecithin: |
| 199 | 30 | 30.6 | 21 | 2 | AAY18481 | Aay18481 Lecithin: |
| 200 | 30 | 30.6 | 21 | 8 | ADG20961 | Adg20961 Apolipopr |
| 201 | 30 | 30.6 | 21 | 8 | ADJ32903 | Adj32903 Apo lipop |
| 202 | 30 | 30.6 | 22 | 2 | AAY18742 | Aay18742 Lecithin: |
| 203 | 30 | 30.6 | 22 | 2 | AAY18731 | Aay18731 Lecithin: |
| 204 | 30 | 30.6 | 22 | 2 | AAY18796 | Aay18796 Lecithin: |
| 205 | 30 | 30.6 | 22 | 2 | AAY18773 | Aay18773 Lecithin: |
| 206 | 30 | 30.6 | 22 | 2 | AAY18757 | Aay18757 Lecithin: |
| 207 | 30 | 30.6 | 22 | 2 | AAY18795 | Aay18795 Lecithin: |
| 208 | 30 | 30.6 | 22 | 2 | AAY18723 | Aay18723 Lecithin: |
| 209 | 30 | 30.6 | 22 | 2 | AAY18724 | Aay18724 Lecithin: |
| 210 | 30 | 30.6 | 22 | 2 | AAY18725 | Aay18725 Lecithin: |
| 211 | 30 | 30.6 | 22 | 2 | AAY18753 | Aay18753 Lecithin: |
| 212 | 30 | 30.6 | 22 | 2 | AAY18798 | Aay18798 Lecithin: |
| 213 | 30 | 30.6 | 22 | 2 | AAY18794 | Aay18794 Lecithin: |
| 214 | 30 | 30.6 | 22 | 2 | AAY18740 | Aay18740 Lecithin: |
| 215 | 30 | 30.6 | 22 | 2 | AAY18792 | Aay18792 Lecithin: |
| 216 | 30 | 30.6 | 22 | 2 | AAY18748 | Aay18748 Lecithin: |
| 217 | 30 | 30.6 | 22 | 2 | AAY18752 | Aay18752 Lecithin: |
| 218 | 30 | 30.6 | 22 | 2 | AAY18756 | Aay18756 Lecithin: |
| 219 | 30 | 30.6 | 22 | 2 | AAY19052 | Aay19052 Lecithin: |
| 220 | 30 | 30.6 | 22 | 2 | AAY18977 | Aay18977 Lecithin: |
| 221 | 30 | 30.6 | 22 | 2 | AAY19027 | Aay19027 Lecithin: |
| 222 | 30 | 30.6 | 22 | 2 | AAY18978 | Aay18978 Lecithin: |
| 223 | 30 | 30.6 | 22 | 2 | AAY19007 | Aay19007 Lecithin: |
| 224 | 30 | 30.6 | 22 | 2 | AAY19049 | Aay19049 Lecithin: |
| 225 | 30 | 30.6 | 22 | 2 | AAY18996 | Aay18996 Lecithin: |
| 226 | 30 | 30.6 | 22 | 2 | AAY19006 | Aay19006 Lecithin: |
| 227 | 30 | 30.6 | 22 | 2 | AAY19011 | Aay19011 Lecithin: |
| 228 | 30 | 30.6 | 22 | 2 | AAY19002 | Aay19002 Lecithin: |
| 229 | 30 | 30.6 | 22 | 2 | AAY19050 | Aay19050 Lecithin: |
| 230 | 30 | 30.6 | 22 | 2 | AAY18985 | Aay18985 Lecithin: |
| 231 | 30 | 30.6 | 22 | 2 | AAY19010 | Aay19010 Lecithin: |
| 232 | 30 | 30.6 | 22 | 2 | AAY19046 | Aay19046 Lecithin: |
| 233 | 30 | 30.6 | 22 | 2 | AAY18979 | Aay18979 Lecithin: |
| 234 | 30 | 30.6 | 22 | 2 | AAY18994 | Aay18994 Lecithin: |
| 235 | 30 | 30.6 | 22 | 2 | AAY19048 | Aay19048 Lecithin: |
| 236 | 30 | 30.6 | 22 | 2 | AAY19256 | Aay19256 Lecithin: |
| 237 | 30 | 30.6 | 22 | 2 | AAY19302 | Aay19302 Lecithin: |
| 238 | 30 | 30.6 | 22 | 2 | AAY19260 | Aay19260 Lecithin: |
| 239 | 30 | 30.6 | 22 | 2 | AAY19281 | Aay19281 Lecithin: |
| 240 | 30 | 30.6 | 22 | 2 | AAY19233 | Aay19233 Lecithin: |
| 241 | 30 | 30.6 | 22 | 2 | AAY19304 | Aay19304 Lecithin: |
| 242 | 30 | 30.6 | 22 | 2 | AAY19232 | Aay19232 Lecithin: |
| 243 | 30 | 30.6 | 22 | 2 | AAY19261 | Aay19261 Lecithin: |
| 244 | 30 | 30.6 | 22 | 2 | AAY19265 | Aay19265 Lecithin: |
| 245 | 30 | 30.6 | 22 | 2 | AAY19300 | Aay19300 Lecithin: |
| 246 | 30 | 30.6 | 22 | 2 | AAY19264 | Aay19264 Lecithin: |
| 247 | 30 | 30.6 | 22 | 2 | AAY19231 | Aay19231 Lecithin: |
| 248 | 30 | 30.6 | 22 | 2 | AAY19306 | Aay19306 Lecithin: |
| 249 | 30 | 30.6 | 22 | 2 | AAY19239 | Aay19239 Lecithin: |
| 250 | 30 | 30.6 | 22 | 2 | AAY19248 | Aay19248 Lecithin: |
| 251 | 30 | 30.6 | 22 | 2 | AAY19250 | Aay19250 Lecithin: |
| 252 | 30 | 30.6 | 22 | 2 | AAY19303 | Aay19303 Lecithin: |
| 253 | 30 | 30.6 | 22 | 2 | AAY18533 | Aay18533 Lecithin: |
| 254 | 30 | 30.6 | 22 | 2 | AAY18529 | Aay18529 Lecithin: |
| 255 | 30 | 30.6 | 22 | 2 | AAY18494 | Aay18494 Lecithin: |
| 256 | 30 | 30.6 | 22 | 2 | AAY18489 | Aay18489 Lecithin: |

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|---|---|---|---|---|---|---|
| 257 | 30 | 30.6 | 22 | 2 | AAY18479 | Aay18479 Lecithin: |
| 258 | 30 | 30.6 | 22 | 2 | AAY18490 | Aay18490 Lecithin: |
| 259 | 30 | 30.6 | 22 | 2 | AAY18535 | Aay18535 Lecithin: |
| 260 | 30 | 30.6 | 22 | 2 | AAY18493 | Aay18493 Lecithin: |
| 261 | 30 | 30.6 | 22 | 2 | AAY18510 | Aay18510 Lecithin: |
| 262 | 30 | 30.6 | 22 | 2 | AAY18460 | Aay18460 Lecithin: |
| 263 | 30 | 30.6 | 22 | 2 | AAY18461 | Aay18461 Lecithin: |
| 264 | 30 | 30.6 | 22 | 2 | AAY18531 | Aay18531 Lecithin: |
| 265 | 30 | 30.6 | 22 | 2 | AAY18532 | Aay18532 Lecithin: |
| 266 | 30 | 30.6 | 22 | 2 | AAY18485 | Aay18485 Lecithin: |
| 267 | 30 | 30.6 | 22 | 2 | AAY18462 | Aay18462 Lecithin: |
| 268 | 30 | 30.6 | 22 | 2 | AAY18468 | Aay18468 Lecithin: |
| 269 | 30 | 30.6 | 22 | 2 | AAY18477 | Aay18477 Lecithin: |
| 270 | 30 | 30.6 | 22 | 8 | ADG20948 | Adg20948 Apolipopr |
| 271 | 30 | 30.6 | 22 | 8 | ADG20965 | Adg20965 Apolipopr |
| 272 | 30 | 30.6 | 22 | 8 | ADG20969 | Adg20969 Apolipopr |
| 273 | 30 | 30.6 | 22 | 8 | ADG20942 | Adg20942 Apolipopr |
| 274 | 30 | 30.6 | 22 | 8 | ADG20973 | Adg20973 Apolipopr |
| 275 | 30 | 30.6 | 22 | 8 | ADG21009 | Adg21009 Apolipopr |
| 276 | 30 | 30.6 | 22 | 8 | ADG20941 | Adg20941 Apolipopr |
| 277 | 30 | 30.6 | 22 | 8 | ADG20974 | Adg20974 Apolipopr |
| 278 | 30 | 30.6 | 22 | 8 | ADG21012 | Adg21012 Apolipopr |
| 279 | 30 | 30.6 | 22 | 8 | ADG21015 | Adg21015 Apolipopr |
| 280 | 30 | 30.6 | 22 | 8 | ADG20959 | Adg20959 Apolipopr |
| 281 | 30 | 30.6 | 22 | 8 | ADG21011 | Adg21011 Apolipopr |
| 282 | 30 | 30.6 | 22 | 8 | ADG20970 | Adg20970 Apolipopr |
| 283 | 30 | 30.6 | 22 | 8 | ADG20940 | Adg20940 Apolipopr |
| 284 | 30 | 30.6 | 22 | 8 | ADG20957 | Adg20957 Apolipopr |
| 285 | 30 | 30.6 | 22 | 8 | ADG20990 | Adg20990 Apolipopr |
| 286 | 30 | 30.6 | 22 | 8 | ADG21013 | Adg21013 Apolipopr |
| 287 | 30 | 30.6 | 22 | 8 | ADJ32955 | Adj32955 Apo lipop |
| 288 | 30 | 30.6 | 22 | 8 | ADJ32884 | Adj32884 Apo lipop |
| 289 | 30 | 30.6 | 22 | 8 | ADJ32953 | Adj32953 Apo lipop |
| 290 | 30 | 30.6 | 22 | 8 | ADJ32899 | Adj32899 Apo lipop |
| 291 | 30 | 30.6 | 22 | 8 | ADJ32890 | Adj32890 Apo lipop |
| 292 | 30 | 30.6 | 22 | 8 | ADJ32882 | Adj32882 Apo lipop |
| 293 | 30 | 30.6 | 22 | 8 | ADJ32907 | Adj32907 Apo lipop |
| 294 | 30 | 30.6 | 22 | 8 | ADJ32883 | Adj32883 Apo lipop |
| 295 | 30 | 30.6 | 22 | 8 | ADJ32951 | Adj32951 Apo lipop |
| 296 | 30 | 30.6 | 22 | 8 | ADJ32911 | Adj32911 Apo lipop |
| 297 | 30 | 30.6 | 22 | 8 | ADJ32901 | Adj32901 Apo lipop |
| 298 | 30 | 30.6 | 22 | 8 | ADJ32916 | Adj32916 Apo lipop |
| 299 | 30 | 30.6 | 22 | 8 | ADJ32912 | Adj32912 Apo lipop |
| 300 | 30 | 30.6 | 22 | 8 | ADJ32954 | Adj32954 Apo lipop |
| 301 | 30 | 30.6 | 22 | 8 | ADJ32915 | Adj32915 Apo lipop |
| 302 | 30 | 30.6 | 22 | 8 | ADJ32932 | Adj32932 Apo lipop |
| 303 | 30 | 30.6 | 22 | 8 | ADJ32957 | Adj32957 Apo lipop |
| 304 | 30 | 30.6 | 24 | 10 | AEE38455 | Aee38455 Human ser |
| 305 | 30 | 30.6 | 25 | 2 | AAR36467 | Aar36467 DFI-22.2( |
| 306 | 30 | 30.6 | 25 | 2 | AAR51815 | Aar51815 Der f I d |
| 307 | 30 | 30.6 | 25 | 2 | AAR77119 | Aar77119 Dermatoph |
| 308 | 30 | 30.6 | 25 | 2 | AAW71898 | Aaw71898 Dermatoph |
| 309 | 30 | 30.6 | 25 | 2 | AAY50444 | Aay50444 Dermatoph |
| 310 | 30 | 30.6 | 25 | 4 | AAU19047 | Aau19047 T-cell ep |
| 311 | 30 | 30.6 | 25 | 6 | ABP97152 | Abp97152 Smad3C fr |
| 312 | 30 | 30.6 | 25 | 6 | ABP97153 | Abp97153 Smad3C fr |
| 313 | 30 | 30.6 | 27 | 3 | AAB29253 | Aab29253 Mouse cyc |
| 314 | 30 | 30.6 | 27 | 3 | AAY43808 | Aay43808 Cyclin de |
| 315 | 30 | 30.6 | 27 | 4 | AAB62207 | Aab62207 Mouse cyc |
| 316 | 30 | 30.6 | 27 | 4 | AAB67682 | Aab67682 Cyclin de |
| 317 | 30 | 30.6 | 27 | 4 | AAM52559 | Aam52559 Murine cy |

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|---|---|---|---|---|---|---|
| 318 | 30 | 30.6 | 27 | 4 | AAB74488 | Aab74488 Murine cy |
| 319 | 30 | 30.6 | 27 | 4 | AAB82393 | Aab82393 Mouse cyc |
| 320 | 30 | 30.6 | 27 | 4 | AAB74462 | Aab74462 Murine cy |
| 321 | 30 | 30.6 | 27 | 4 | AAG62584 | Aag62584 Murine cy |
| 322 | 30 | 30.6 | 27 | 4 | AAB84850 | Aab84850 Murine cy |
| 323 | 30 | 30.6 | 27 | 4 | AAE09727 | Aae09727 Destructi |
| 324 | 30 | 30.6 | 27 | 6 | ABR39541 | Abr39541 Mouse cyc |
| 325 | 30 | 30.6 | 27 | 6 | ABG73727 | Abg73727 Murine cy |
| 326 | 30 | 30.6 | 27 | 6 | ADA07077 | Ada07077 Mouse cyc |
| 327 | 30 | 30.6 | 27 | 7 | ADF90359 | Adf90359 Mouse Cyc |
| 328 | 30 | 30.6 | 27 | 7 | ADH69411 | Adh69411 Mouse cyc |
| 329 | 30 | 30.6 | 27 | 8 | ADO26208 | Ado26208 Mouse cyc |
| 330 | 30 | 30.6 | 27 | 9 | ADY97775 | Ady97775 Mouse cyc |
| 331 | 30 | 30.6 | 29 | 2 | AAR36466 | Aar36466 DFI-22.1( |
| 332 | 30 | 30.6 | 29 | 2 | AAR36468 | Aar36468 DFI-22.4( |
| 333 | 30 | 30.6 | 29 | 2 | AAR51814 | Aar51814 Der f I d |
| 334 | 30 | 30.6 | 29 | 2 | AAR51816 | Aar51816 Der f I d |
| 335 | 30 | 30.6 | 29 | 2 | AAW71990 | Aaw71990 Dermatoph |
| 336 | 30 | 30.6 | 29 | 2 | AAW71989 | Aaw71989 Dermatoph |
| 337 | 30 | 30.6 | 29 | 2 | AAY50445 | Aay50445 Dermatoph |
| 338 | 30 | 30.6 | 29 | 2 | AAY50443 | Aay50443 Dermatoph |
| 339 | 30 | 30.6 | 29 | 4 | AAU19048 | Aau19048 T-cell ep |
| 340 | 30 | 30.6 | 29 | 4 | AAU19046 | Aau19046 T-cell ep |
| 341 | 30 | 30.6 | 29 | 4 | AAE05049 | Aae05049 Human ZCY |
| 342 | 30 | 30.6 | 29 | 7 | ABR83686 | Abr83686 Human IL- |
| 343 | 30 | 30.6 | 29 | 7 | ADH69550 | Adh69550 Human ZCY |
| 344 | 30 | 30.6 | 29 | 10 | AEE36210 | Aee36210 Human ser |
| 345 | 29 | 29.6 | 8 | 5 | ABP53199 | Abp53199 Zinc fing |
| 346 | 29 | 29.6 | 8 | 6 | ABU60745 | Abu60745 Phage dis |
| 347 | 29 | 29.6 | 8 | 7 | ADJ98398 | Adj98398 Zinc fing |
| 348 | 29 | 29.6 | 13 | 6 | ABR62229 | Abr62229 Apolipopr |
| 349 | 29 | 29.6 | 14 | 2 | AAR81162 | Aar81162 Anti-fung |
| 350 | 29 | 29.6 | 14 | 2 | AAR77991 | Aar77991 BPI prote |
| 351 | 29 | 29.6 | 14 | 2 | AAR86531 | Aar86531 BPI.83 fo |
| 352 | 29 | 29.6 | 14 | 2 | AAR76318 | Aar76318 Bacterial |
| 353 | 29 | 29.6 | 14 | 2 | AAW05928 | Aaw05928 Recombina |
| 354 | 29 | 29.6 | 14 | 2 | AAW63379 | Aaw63379 Human BPI |
| 355 | 29 | 29.6 | 14 | 3 | AAB16117 | Aab16117 Bacterici |
| 356 | 29 | 29.6 | 14 | 4 | AAB52287 | Aab52287 Peptide B |
| 357 | 29 | 29.6 | 14 | 8 | ADH68260 | Adh68260 GPCR rela |
| 358 | 29 | 29.6 | 14 | 8 | ADI66579 | Adi66579 Rat bacte |
| 359 | 29 | 29.6 | 15 | 5 | ABP56527 | Abp56527 Human P24 |
| 360 | 29 | 29.6 | 15 | 6 | ABR57623 | Abr57623 Human end |
| 361 | 29 | 29.6 | 15 | 6 | ABB98946 | Abb98946 Translati |
| 362 | 29 | 29.6 | 16 | 2 | AAW47956 | Aaw47956 AE110 ext |
| 363 | 29 | 29.6 | 19 | 4 | ABB43395 | Abb43395 Peptide # |
| 364 | 29 | 29.6 | 19 | 4 | AAM37276 | Aam37276 Peptide # |
| 365 | 29 | 29.6 | 19 | 4 | AAM77147 | Aam77147 Human bon |
| 366 | 29 | 29.6 | 19 | 4 | AAM64319 | Aam64319 Human bra |
| 367 | 29 | 29.6 | 19 | 4 | ABG58772 | Abg58772 Human liv |
| 368 | 29 | 29.6 | 19 | 5 | ABG46158 | Abg46158 Human pep |
| 369 | 29 | 29.6 | 22 | 2 | AAY18712 | Aay18712 Lecithin: |
| 370 | 29 | 29.6 | 22 | 2 | AAY18787 | Aay18787 Lecithin: |
| 371 | 29 | 29.6 | 22 | 2 | AAY18855 | Aay18855 Lecithin: |
| 372 | 29 | 29.6 | 22 | 2 | AAY18806 | Aay18806 Lecithin: |
| 373 | 29 | 29.6 | 22 | 2 | AAY18705 | Aay18705 Lecithin: |
| 374 | 29 | 29.6 | 22 | 2 | AAY18793 | Aay18793 Lecithin: |
| 375 | 29 | 29.6 | 22 | 2 | AAY18760 | Aay18760 Lecithin: |
| 376 | 29 | 29.6 | 22 | 2 | AAY18763 | Aay18763 Lecithin: |
| 377 | 29 | 29.6 | 22 | 2 | AAY19014 | Aay19014 Lecithin: |
| 378 | 29 | 29.6 | 22 | 2 | AAY19109 | Aay19109 Lecithin: |

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|---|---|---|---|---|---|---|
| 379 | 29 | 29.6 | 22 | 2 | AAY19041 | Aay19041 Lecithin: |
| 380 | 29 | 29.6 | 22 | 2 | AAY18966 | Aay18966 Lecithin: |
| 381 | 29 | 29.6 | 22 | 2 | AAY18959 | Aay18959 Lecithin: |
| 382 | 29 | 29.6 | 22 | 2 | AAY19047 | Aay19047 Lecithin: |
| 383 | 29 | 29.6 | 22 | 2 | AAY19017 | Aay19017 Lecithin: |
| 384 | 29 | 29.6 | 22 | 2 | AAY19060 | Aay19060 Lecithin: |
| 385 | 29 | 29.6 | 22 | 2 | AAY19213 | Aay19213 Lecithin: |
| 386 | 29 | 29.6 | 22 | 2 | AAY19268 | Aay19268 Lecithin: |
| 387 | 29 | 29.6 | 22 | 2 | AAY19271 | Aay19271 Lecithin: |
| 388 | 29 | 29.6 | 22 | 2 | AAY19314 | Aay19314 Lecithin: |
| 389 | 29 | 29.6 | 22 | 2 | AAY19363 | Aay19363 Lecithin: |
| 390 | 29 | 29.6 | 22 | 2 | AAY19220 | Aay19220 Lecithin: |
| 391 | 29 | 29.6 | 22 | 2 | AAY19295 | Aay19295 Lecithin: |
| 392 | 29 | 29.6 | 22 | 2 | AAY19301 | Aay19301 Lecithin: |
| 393 | 29 | 29.6 | 22 | 2 | AAY18524 | Aay18524 Lecithin: |
| 394 | 29 | 29.6 | 22 | 2 | AAY18500 | Aay18500 Lecithin: |
| 395 | 29 | 29.6 | 22 | 2 | AAY18449 | Aay18449 Lecithin: |
| 396 | 29 | 29.6 | 22 | 2 | AAY18530 | Aay18530 Lecithin: |
| 397 | 29 | 29.6 | 22 | 2 | AAY18543 | Aay18543 Lecithin: |
| 398 | 29 | 29.6 | 22 | 2 | AAY18592 | Aay18592 Lecithin: |
| 399 | 29 | 29.6 | 22 | 2 | AAY18442 | Aay18442 Lecithin: |
| 400 | 29 | 29.6 | 22 | 2 | AAY18497 | Aay18497 Lecithin: |
| 401 | 29 | 29.6 | 22 | 8 | ADG21072 | Adg21072 Apolipopr |
| 402 | 29 | 29.6 | 22 | 8 | ADG20929 | Adg20929 Apolipopr |
| 403 | 29 | 29.6 | 22 | 8 | ADG21023 | Adg21023 Apolipopr |
| 404 | 29 | 29.6 | 22 | 8 | ADG21004 | Adg21004 Apolipopr |
| 405 | 29 | 29.6 | 22 | 8 | ADG20977 | Adg20977 Apolipopr |
| 406 | 29 | 29.6 | 22 | 8 | ADG20922 | Adg20922 Apolipopr |
| 407 | 29 | 29.6 | 22 | 8 | ADG21010 | Adg21010 Apolipopr |
| 408 | 29 | 29.6 | 22 | 8 | ADG20980 | Adg20980 Apolipopr |
| 409 | 29 | 29.6 | 22 | 8 | ADJ32946 | Adj32946 Apo lipop |
| 410 | 29 | 29.6 | 22 | 8 | ADJ32919 | Adj32919 Apo lipop |
| 411 | 29 | 29.6 | 22 | 8 | ADJ32965 | Adj32965 Apo lipop |
| 412 | 29 | 29.6 | 22 | 8 | ADJ32871 | Adj32871 Apo lipop |
| 413 | 29 | 29.6 | 22 | 8 | ADJ32864 | Adj32864 Apo lipop |
| 414 | 29 | 29.6 | 22 | 8 | ADJ32922 | Adj32922 Apo lipop |
| 415 | 29 | 29.6 | 22 | 8 | ADJ32952 | Adj32952 Apo lipop |
| 416 | 29 | 29.6 | 22 | 8 | ADJ33014 | Adj33014 Apo lipop |
| 417 | 29 | 29.6 | 22 | 8 | ADT39374 | Adt39374 hSARS vir |
| 418 | 29 | 29.6 | 22 | 8 | ADS78794 | Ads78794 SARS viru |
| 419 | 29 | 29.6 | 22 | 8 | ADT36904 | Adt36904 hSARS vir |
| 420 | 29 | 29.6 | 23 | 7 | ADL33660 | Adl33660 Mutated z |
| 421 | 29 | 29.6 | 23 | 7 | ADL33631 | Adl33631 Mutated z |
| 422 | 29 | 29.6 | 24 | 2 | AAY21285 | Aay21285 Human sem |
| 423 | 29 | 29.6 | 24 | 4 | AAB81887 | Aab81887 Nerve cel |
| 424 | 29 | 29.6 | 24 | 9 | ADV99788 | Adv99788 Glucanase |
| 425 | 29 | 29.6 | 25 | 10 | AEE37290 | Aee37290 Human ser |
| 426 | 29 | 29.6 | 26 | 4 | ABB37713 | Abb37713 Peptide # |
| 427 | 29 | 29.6 | 28 | 4 | AAM21751 | Aam21751 Peptide # |
| 428 | 29 | 29.6 | 28 | 4 | ABB44120 | Abb44120 Peptide # |
| 429 | 29 | 29.6 | 28 | 4 | AAM38067 | Aam38067 Peptide # |
| 430 | 29 | 29.6 | 28 | 4 | ABB27007 | Abb27007 Protein # |
| 431 | 29 | 29.6 | 28 | 4 | AAM77847 | Aam77847 Human bon |
| 432 | 29 | 29.6 | 28 | 4 | AAM65142 | Aam65142 Human bra |
| 433 | 29 | 29.6 | 28 | 4 | ABG59502 | Abg59502 Human liv |
| 434 | 29 | 29.6 | 28 | 8 | ADG71882 | Adg71882 Human NOV |
| 435 | 29 | 29.6 | 28 | 8 | ADJ87219 | Adj87219 Human G p |
| 436 | 29 | 29.6 | 28 | 10 | AEE28018 | Aee28018 S. pneumo |
| 437 | 29 | 29.6 | 28 | 10 | AEE28072 | Aee28072 H, influe |
| 438 | 29 | 29.6 | 28 | 10 | AEF10501 | Aef10501 Human NOV |
| 439 | 29 | 29.6 | 29 | 7 | ABW00978 | Abw00978 Mutant Ja |

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|---|---|---|---|---|---|---|
| 440 | 29 | 29.6 | 29 | 7 | ADE86421 | Ade86421 Mutant JA |
| 441 | 29 | 29.6 | 30 | 5 | AAU84858 | Aau84858 Human gp1 |
| 442 | 28.5 | 29.1 | 22 | 2 | AAY18848 | Aay18848 Lecithin: |
| 443 | 28.5 | 29.1 | 22 | 2 | AAY18845 | Aay18845 Lecithin: |
| 444 | 28.5 | 29.1 | 22 | 2 | AAY18862 | Aay18862 Lecithin: |
| 445 | 28.5 | 29.1 | 22 | 2 | AAY19099 | Aay19099 Lecithin: |
| 446 | 28.5 | 29.1 | 22 | 2 | AAY19102 | Aay19102 Lecithin: |
| 447 | 28.5 | 29.1 | 22 | 2 | AAY19116 | Aay19116 Lecithin: |
| 448 | 28.5 | 29.1 | 22 | 2 | AAY19353 | Aay19353 Lecithin: |
| 449 | 28.5 | 29.1 | 22 | 2 | AAY19370 | Aay19370 Lecithin: |
| 450 | 28.5 | 29.1 | 22 | 2 | AAY19356 | Aay19356 Lecithin: |
| 451 | 28.5 | 29.1 | 22 | 2 | AAY18599 | Aay18599 Lecithin: |
| 452 | 28.5 | 29.1 | 22 | 2 | AAY18585 | Aay18585 Lecithin: |
| 453 | 28.5 | 29.1 | 22 | 2 | AAY18582 | Aay18582 Lecithin: |
| 454 | 28.5 | 29.1 | 22 | 8 | ADG21079 | Adg21079 Apolipopr |
| 455 | 28.5 | 29.1 | 22 | 8 | ADG21065 | Adg21065 Apolipopr |
| 456 | 28.5 | 29.1 | 22 | 8 | ADG21062 | Adg21062 Apolipopr |
| 457 | 28.5 | 29.1 | 22 | 8 | ADJ33004 | Adj33004 Apo lipop |
| 458 | 28.5 | 29.1 | 22 | 8 | ADJ33007 | Adj33007 Apo lipop |
| 459 | 28.5 | 29.1 | 22 | 8 | ADJ33021 | Adj33021 Apo lipop |
| 460 | 28.5 | 29.1 | 25 | 2 | AAR73663 | Aar73663 Ac-PDGF(2 |
| 461 | 28 | 28.6 | 7 | 4 | ABB56099 | Abb56099 Vascular |
| 462 | 28 | 28.6 | 7 | 4 | AAU28516 | Aau28516 DPI trypt |
| 463 | 28 | 28.6 | 7 | 4 | AAU24833 | Aau24833 Schizophr |
| 464 | 28 | 28.6 | 7 | 4 | AAU26162 | Aau26162 Depressio |
| 465 | 28 | 28.6 | 7 | 4 | AAU15177 | Aau15177 Schizophr |
| 466 | 28 | 28.6 | 7 | 4 | ABB52072 | Abb52072 Human API |
| 467 | 28 | 28.6 | 7 | 5 | ABG78630 | Abg78630 Multiple |
| 468 | 28 | 28.6 | 7 | 6 | ABR58923 | Abr58923 Alzheimer |
| 469 | 28 | 28.6 | 7 | 8 | ADN32135 | Adn32135 Human Alz |
| 470 | 28 | 28.6 | 7 | 8 | ADO78444 | Ado78444 Schizophr |
| 471 | 28 | 28.6 | 8 | 8 | ADK10579 | Adk10579 Human pap |
| 472 | 28 | 28.6 | 10 | 4 | AAG87262 | Aag87262 Saccharom |
| 473 | 28 | 28.6 | 10 | 8 | ADK10596 | Adk10596 Human pap |
| 474 | 28 | 28.6 | 12 | 9 | ADY81626 | Ady81626 HIV-1 ant |
| 475 | 28 | 28.6 | 12 | 9 | ADY81627 | Ady81627 HIV-1 ant |
| 476 | 28 | 28.6 | 13 | 3 | AAY88906 | Aay88906 Core poly |
| 477 | 28 | 28.6 | 13 | 4 | AAB77261 | Aab77261 Core poly |
| 478 | 28 | 28.6 | 13 | 4 | ABB00265 | Abb00265 Viral DP1 |
| 479 | 28 | 28.6 | 13 | 4 | ABB01739 | Abb01739 Viral cor |
| 480 | 28 | 28.6 | 13 | 4 | AAU12814 | Aau12814 DP178-lik |
| 481 | 28 | 28.6 | 13 | 5 | ADE01759 | Ade01759 Hybrid po |
| 482 | 28 | 28.6 | 13 | 6 | ABO10308 | Abo10308 HPIV3 F1 |
| 483 | 28 | 28.6 | 13 | 6 | ABP68027 | Abp68027 Bacillus |
| 484 | 28 | 28.6 | 13 | 9 | ADY81628 | Ady81628 HIV-1 ant |
| 485 | 28 | 28.6 | 13 | 9 | AEA24073 | Aea24073 Human pro |
| 486 | 28 | 28.6 | 14 | 2 | AAW22990 | Aaw22990 Human ser |
| 487 | 28 | 28.6 | 14 | 9 | ADY81646 | Ady81646 HIV-1 ant |
| 488 | 28 | 28.6 | 14 | 9 | ADY81598 | Ady81598 HIV-1 ant |
| 489 | 28 | 28.6 | 14 | 9 | ADY81629 | Ady81629 HIV-1 ant |
| 490 | 28 | 28.6 | 15 | 4 | ABR52288 | Abr52288 IgE-react |
| 491 | 28 | 28.6 | 15 | 4 | ABR51487 | Abr51487 Pen a 1 I |
| 492 | 28 | 28.6 | 15 | 4 | ABR51339 | Abr51339 Shrimp Pe |
| 493 | 28 | 28.6 | 15 | 8 | ADO77295 | Ado77295 Human 213 |
| 494 | 28 | 28.6 | 15 | 8 | ADO77183 | Ado77183 Human 213 |
| 495 | 28 | 28.6 | 15 | 8 | ADO77189 | Ado77189 Human 213 |
| 496 | 28 | 28.6 | 15 | 8 | ADO77269 | Ado77269 Human 213 |
| 497 | 28 | 28.6 | 15 | 8 | ADP26474 | Adp26474 Plasmodiu |
| 498 | 28 | 28.6 | 15 | 9 | ADV21748 | Adv21748 SIV pol p |
| 499 | 28 | 28.6 | 15 | 9 | ADY81631 | Ady81631 HIV-1 ant |
| 500 | 28 | 28.6 | 15 | 9 | ADY81599 | Ady81599 HIV-1 ant |

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|---|---|---|---|---|---|---|
| 501 | 28 | 28.6 | 15 | 9 | ADY81647 | Ady81647 HIV-1 ant |
| 502 | 28 | 28.6 | 15 | 9 | ADY81630 | Ady81630 HIV-1 ant |
| 503 | 28 | 28.6 | 15 | 9 | ADY81648 | Ady81648 HIV-1 ant |
| 504 | 28 | 28.6 | 16 | 2 | AAW70134 | Aaw70134 Peptide p |
| 505 | 28 | 28.6 | 16 | 4 | AAE05591 | Aae05591 N-termina |
| 506 | 28 | 28.6 | 16 | 6 | ABO43454 | Abo43454 M. tuberc |
| 507 | 28 | 28.6 | 16 | 9 | ADY81600 | Ady81600 HIV-1 ant |
| 508 | 28 | 28.6 | 16 | 9 | ADY81649 | Ady81649 HIV-1 ant |
| 509 | 28 | 28.6 | 16 | 9 | ADY81632 | Ady81632 HIV-1 ant |
| 510 | 28 | 28.6 | 17 | 9 | ADY81601 | Ady81601 HIV-1 ant |
| 511 | 28 | 28.6 | 18 | 3 | AAB00146 | Aab00146 Human pro |
| 512 | 28 | 28.6 | 18 | 5 | ABG31672 | Abg31672 Vitamin K |
| 513 | 28 | 28.6 | 18 | 8 | ADI28365 | Adi28365 Human TIE |
| 514 | 28 | 28.6 | 18 | 9 | ADV67399 | Adv67399 Amino aci |
| 515 | 28 | 28.6 | 19 | 7 | ADC98804 | Adc98804 Streptoco |
| 516 | 28 | 28.6 | 19 | 7 | ADF14672 | Adf14672 Rheumatoi |
| 517 | 28 | 28.6 | 19 | 9 | AED27832 | Aed27832 Guanylate |
| 518 | 28 | 28.6 | 20 | 2 | AAW33933 | Aaw33933 D2 dopami |
| 519 | 28 | 28.6 | 20 | 4 | ABB36881 | Abb36881 Peptide # |
| 520 | 28 | 28.6 | 20 | 4 | AAM70031 | Aam70031 Human bon |
| 521 | 28 | 28.6 | 20 | 4 | AAM57628 | Aam57628 Human bra |
| 522 | 28 | 28.6 | 20 | 4 | AAM05511 | Aam05511 Peptide # |
| 523 | 28 | 28.6 | 20 | 5 | ABG39662 | Abg39662 Human pep |
| 524 | 28 | 28.6 | 20 | 6 | ABP55288 | Abp55288 Human adr |
| 525 | 28 | 28.6 | 20 | 6 | ABP55287 | Abp55287 Human dop |
| 526 | 28 | 28.6 | 20 | 8 | ABO58184 | Abo58184 Human gen |
| 527 | 28 | 28.6 | 20 | 9 | ADW52426 | Adw52426 Human PL |
| 528 | 28 | 28.6 | 21 | 2 | AAR36449 | Aar36449 DFI-4(40- |
| 529 | 28 | 28.6 | 21 | 2 | AAR51797 | Aar51797 Der f I d |
| 530 | 28 | 28.6 | 21 | 2 | AAW71972 | Aaw71972 Dermatoph |
| 531 | 28 | 28.6 | 21 | 2 | AAY50426 | Aay50426 Dermatoph |
| 532 | 28 | 28.6 | 21 | 4 | AAU19029 | Aau19029 T-cell ep |
| 533 | 28 | 28.6 | 21 | 5 | ABG60820 | Abg60820 Cellular |
| 534 | 28 | 28.6 | 21 | 6 | ABB82879 | Abb82879 Dopamine |
| 535 | 28 | 28.6 | 21 | 8 | ADT39739 | Adt39739 hSARS vir |
| 536 | 28 | 28.6 | 21 | 8 | ADS79158 | Ads79158 SARS viru |
| 537 | 28 | 28.6 | 21 | 8 | ADT37269 | Adt37269 hSARS vir |
| 538 | 28 | 28.6 | 21 | 8 | ABY03652 | Aby03652 SARS coro |
| 539 | 28 | 28.6 | 21 | 9 | ADY62294 | Ady62294 Human RHA |
| 540 | 28 | 28.6 | 21 | 9 | ADY96582 | Ady96582 RHAMM rel |
| 541 | 28 | 28.6 | 21 | 9 | ADZ11922 | Adz11922 Human RHA |
| 542 | 28 | 28.6 | 22 | 2 | AAY18782 | Aay18782 Lecithin: |
| 543 | 28 | 28.6 | 22 | 2 | AAY18777 | Aay18777 Lecithin: |
| 544 | 28 | 28.6 | 22 | 2 | AAY18800 | Aay18800 Lecithin: |
| 545 | 28 | 28.6 | 22 | 2 | AAY18797 | Aay18797 Lecithin: |
| 546 | 28 | 28.6 | 22 | 2 | AAY19031 | Aay19031 Lecithin: |
| 547 | 28 | 28.6 | 22 | 2 | AAY19054 | Aay19054 Lecithin: |
| 548 | 28 | 28.6 | 22 | 2 | AAY19051 | Aay19051 Lecithin: |
| 549 | 28 | 28.6 | 22 | 2 | AAY19036 | Aay19036 Lecithin: |
| 550 | 28 | 28.6 | 22 | 2 | AAY19290 | Aay19290 Lecithin: |
| 551 | 28 | 28.6 | 22 | 2 | AAY19285 | Aay19285 Lecithin: |
| 552 | 28 | 28.6 | 22 | 2 | AAY19308 | Aay19308 Lecithin: |
| 553 | 28 | 28.6 | 22 | 2 | AAY19305 | Aay19305 Lecithin: |
| 554 | 28 | 28.6 | 22 | 2 | AAY18514 | Aay18514 Lecithin: |
| 555 | 28 | 28.6 | 22 | 2 | AAY18519 | Aay18519 Lecithin: |
| 556 | 28 | 28.6 | 22 | 2 | AAY18537 | Aay18537 Lecithin: |
| 557 | 28 | 28.6 | 22 | 2 | AAY18534 | Aay18534 Lecithin: |
| 558 | 28 | 28.6 | 22 | 8 | ADG20994 | Adg20994 Apolipopr |
| 559 | 28 | 28.6 | 22 | 8 | ADG21014 | Adg21014 Apolipopr |
| 560 | 28 | 28.6 | 22 | 8 | ADG20999 | Adg20999 Apolipopr |
| 561 | 28 | 28.6 | 22 | 8 | ADG21017 | Adg21017 Apolipopr |

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|---|---|---|---|---|---|---|
| 562 | 28 | 28.6 | 22 | 8 | ADJ32956 | Adj32956 Apo lipop |
| 563 | 28 | 28.6 | 22 | 8 | ADJ32936 | Adj32936 Apo lipop |
| 564 | 28 | 28.6 | 22 | 8 | ADJ32959 | Adj32959 Apo lipop |
| 565 | 28 | 28.6 | 22 | 8 | ADJ32941 | Adj32941 Apo lipop |
| 566 | 28 | 28.6 | 22 | 10 | AEE91990 | Aee91990 Polynucle |
| 567 | 28 | 28.6 | 23 | 2 | AAR50814 | Aar50814 G-protein |
| 568 | 28 | 28.6 | 23 | 2 | AAR89195 | Aar89195 GPR adren |
| 569 | 28 | 28.6 | 23 | 2 | AAW02746 | Aaw02746 G-protein |
| 570 | 28 | 28.6 | 24 | 2 | AAW33926 | Aaw33926 D2 dopami |
| 571 | 28 | 28.6 | 24 | 2 | AAW39994 | Aaw39994 Peptide e |
| 572 | 28 | 28.6 | 25 | 2 | AAW40243 | Aaw40243 H. pylori |
| 573 | 28 | 28.6 | 25 | 2 | AAY27802 | Aay27802 Human sec |
| 574 | 28 | 28.6 | 25 | 6 | ABB82545 | Abb82545 Transport |
| 575 | 28 | 28.6 | 25 | 6 | ABO14294 | Abo14294 Novel hum |
| 576 | 28 | 28.6 | 25 | 8 | ADG78702 | Adg78702 Human sec |
| 577 | 28 | 28.6 | 25 | 8 | ADN60992 | Adn60992 Human sec |
| 578 | 28 | 28.6 | 26 | 4 | AAO04818 | Aao04818 Human pol |
| 579 | 28 | 28.6 | 28 | 10 | AEE28038 | Aee28038 S.aureus |
| 580 | 28 | 28.6 | 29 | 3 | AAY89018 | Aay89018 Core poly |
| 581 | 28 | 28.6 | 29 | 3 | AAB08357 | Aab08357 Amino aci |
| 582 | 28 | 28.6 | 29 | 4 | AAB77373 | Aab77373 Core poly |
| 583 | 28 | 28.6 | 29 | 4 | ABB01851 | Abb01851 Viral cor |
| 584 | 28 | 28.6 | 29 | 4 | ABB00377 | Abb00377 Viral DP1 |
| 585 | 28 | 28.6 | 29 | 4 | AAU12926 | Aau12926 DP178-lik |
| 586 | 28 | 28.6 | 29 | 5 | ADE01871 | Ade01871 Hybrid po |
| 587 | 28 | 28.6 | 29 | 6 | ABO10310 | Abo10310 HPIV3 F1 |
| 588 | 28 | 28.6 | 30 | 3 | AAY99896 | Aay99896 Peptide e |
| 589 | 28 | 28.6 | 30 | 5 | AAM49591 | Aam49591 Human bet |
| 590 | 27.5 | 28.1 | 20 | 8 | ADU20811 | Adu20811 Random st |
| 591 | 27.5 | 28.1 | 26 | 4 | AAM77099 | Aam77099 Human bon |
| 592 | 27.5 | 28.1 | 26 | 4 | ABG58743 | Abg58743 Human liv |
| 593 | 27.5 | 28.1 | 30 | 2 | AAR60067 | Aar60067 Antimicro |
| 594 | 27 | 27.6 | 9 | 2 | AAR73669 | Aar73669 Labelled |
| 595 | 27 | 27.6 | 9 | 2 | AAR73652 | Aar73652 Ac-PDGF(7 |
| 596 | 27 | 27.6 | 9 | 2 | AAR73651 | Aar73651 PDGF(73-8 |
| 597 | 27 | 27.6 | 9 | 4 | AAB75780 | Aab75780 HLA class |
| 598 | 27 | 27.6 | 10 | 2 | AAR73653 | Aar73653 PDGF(73-8 |
| 599 | 27 | 27.6 | 10 | 2 | AAR73670 | Aar73670 Labelled |
| 600 | 27 | 27.6 | 10 | 2 | AAR73654 | Aar73654 Ac-PDGF(7 |
| 601 | 27 | 27.6 | 10 | 2 | AAW76008 | Aaw76008 LM609 gra |
| 602 | 27 | 27.6 | 10 | 4 | AAB75788 | Aab75788 HLA class |
| 603 | 27 | 27.6 | 10 | 4 | AAB61366 | Aab61366 LM609 VH |
| 604 | 27 | 27.6 | 10 | 6 | ABO19804 | Abo19804 LM609 hea |
| 605 | 27 | 27.6 | 10 | 7 | ADG71810 | Adg71810 Modified |
| 606 | 27 | 27.6 | 10 | 8 | ADJ57991 | Adj57991 Murine LM |
| 607 | 27 | 27.6 | 10 | 8 | ABY01363 | Aby01363 SARS coro |
| 608 | 27 | 27.6 | 10 | 8 | ABY01202 | Aby01202 SARS coro |
| 609 | 27 | 27.6 | 11 | 4 | AAU28745 | Aau28745 DPI trypt |
| 610 | 27 | 27.6 | 11 | 4 | AAU26393 | Aau26393 Depressio |
| 611 | 27 | 27.6 | 11 | 4 | ABB52317 | Abb52317 Human API |
| 612 | 27 | 27.6 | 11 | 4 | ABB52301 | Abb52301 Human API |
| 613 | 27 | 27.6 | 11 | 4 | ABB52371 | Abb52371 Human API |
| 614 | 27 | 27.6 | 11 | 4 | ABB52409 | Abb52409 Human API |
| 615 | 27 | 27.6 | 11 | 6 | ABP57132 | Abp57132 Breast ca |
| 616 | 27 | 27.6 | 11 | 6 | ABR58785 | Abr58785 Alzheimer |
| 617 | 27 | 27.6 | 11 | 8 | ADN32058 | Adn32058 Human Alz |
| 618 | 27 | 27.6 | 11 | 9 | AEA45350 | Aea45350 Apolipopr |
| 619 | 27 | 27.6 | 11 | 10 | AEF40671 | Aef40671 Pregnancy |
| 620 | 27 | 27.6 | 12 | 8 | ADO06896 | Ado06896 Porcine r |
| 621 | 27 | 27.6 | 13 | 4 | AAU04993 | Aau04993 N-termina |
| 622 | 27 | 27.6 | 13 | 5 | AAU86053 | Aau86053 Human glu |

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|---|---|---|---|---|---|---|
| 623 | 27 | 27.6 | 13 | 6 | ABP68026 | Abp68026 Bacillus |
| 624 | 27 | 27.6 | 13 | 6 | ABP68023 | Abp68023 Bacillus |
| 625 | 27 | 27.6 | 13 | 6 | ABP68021 | Abp68021 Bacillus |
| 626 | 27 | 27.6 | 13 | 6 | ABP68022 | Abp68022 Bacillus |
| 627 | 27 | 27.6 | 13 | 6 | ADA43078 | Ada43078 HLA-DR be |
| 628 | 27 | 27.6 | 13 | 10 | AEF02148 | Aef02148 Ii-key hy |
| 629 | 27 | 27.6 | 14 | 2 | AAR63742 | Aar63742 BPI deriv |
| 630 | 27 | 27.6 | 14 | 2 | AAR61414 | Aar61414 PDGF-B re |
| 631 | 27 | 27.6 | 14 | 2 | AAR81303 | Aar81303 Anti-fung |
| 632 | 27 | 27.6 | 14 | 2 | AAR81302 | Aar81302 Anti-fung |
| 633 | 27 | 27.6 | 14 | 2 | AAR81119 | Aar81119 Anti-fung |
| 634 | 27 | 27.6 | 14 | 2 | AAR78132 | Aar78132 Bacterial |
| 635 | 27 | 27.6 | 14 | 2 | AAR78133 | Aar78133 Bacterial |
| 636 | 27 | 27.6 | 14 | 2 | AAR75995 | Aar75995 BPI prote |
| 637 | 27 | 27.6 | 14 | 2 | AAR82373 | Aar82373 BPI.269, |
| 638 | 27 | 27.6 | 14 | 2 | AAR82372 | Aar82372 BPI.268, |
| 639 | 27 | 27.6 | 14 | 2 | AAR87872 | Aar87872 BPI.268 f |
| 640 | 27 | 27.6 | 14 | 2 | AAR86489 | Aar86489 BPI.32 fo |
| 641 | 27 | 27.6 | 14 | 2 | AAR87873 | Aar87873 BPI.269 f |
| 642 | 27 | 27.6 | 14 | 2 | AAR76277 | Aar76277 Bacterial |
| 643 | 27 | 27.6 | 14 | 2 | AAR76452 | Aar76452 Bacterial |
| 644 | 27 | 27.6 | 14 | 2 | AAW06067 | Aaw06067 Recombina |
| 645 | 27 | 27.6 | 14 | 2 | AAW06068 | Aaw06068 Recombina |
| 646 | 27 | 27.6 | 14 | 2 | AAW05886 | Aaw05886 Recombina |
| 647 | 27 | 27.6 | 14 | 2 | AAW04069 | Aaw04069 Antifunga |
| 648 | 27 | 27.6 | 14 | 2 | AAW04143 | Aaw04143 Antifunga |
| 649 | 27 | 27.6 | 14 | 2 | AAW04142 | Aaw04142 Antifunga |
| 650 | 27 | 27.6 | 14 | 2 | AAW44406 | Aaw44406 Anti-fung |
| 651 | 27 | 27.6 | 14 | 2 | AAW44508 | Aaw44508 Anti-fung |
| 652 | 27 | 27.6 | 14 | 2 | AAW44507 | Aaw44507 Anti-fung |
| 653 | 27 | 27.6 | 14 | 2 | AAW43694 | Aaw43694 Bacterici |
| 654 | 27 | 27.6 | 14 | 2 | AAW43589 | Aaw43589 Bacterici |
| 655 | 27 | 27.6 | 14 | 2 | AAW43693 | Aaw43693 Bacterici |
| 656 | 27 | 27.6 | 14 | 2 | AAW58654 | Aaw58654 Platelet |
| 657 | 27 | 27.6 | 14 | 2 | AAW63518 | Aaw63518 Human BPI |
| 658 | 27 | 27.6 | 14 | 2 | AAW63519 | Aaw63519 Human BPI |
| 659 | 27 | 27.6 | 14 | 2 | AAW63337 | Aaw63337 Human BPI |
| 660 | 27 | 27.6 | 14 | 2 | AAY01187 | Aay01187 Polypepti |
| 661 | 27 | 27.6 | 14 | 2 | AAY00485 | Aay00485 Antifunga |
| 662 | 27 | 27.6 | 14 | 2 | AAY00383 | Aay00383 Antifunga |
| 663 | 27 | 27.6 | 14 | 2 | AAY00484 | Aay00484 Antifunga |
| 664 | 27 | 27.6 | 14 | 3 | AAB16258 | Aab16258 Bacterici |
| 665 | 27 | 27.6 | 14 | 3 | AAB16259 | Aab16259 Bacterici |
| 666 | 27 | 27.6 | 14 | 3 | AAB16074 | Aab16074 Bacterici |
| 667 | 27 | 27.6 | 14 | 4 | AAM97026 | Aam97026 Human pep |
| 668 | 27 | 27.6 | 14 | 4 | AAB65408 | Aab65408 Anti-fung |
| 669 | 27 | 27.6 | 14 | 4 | AAB65409 | Aab65409 Anti-fung |
| 670 | 27 | 27.6 | 14 | 4 | AAB65307 | Aab65307 Anti-fung |
| 671 | 27 | 27.6 | 14 | 4 | AAB68706 | Aab68706 Peptide-b |
| 672 | 27 | 27.6 | 14 | 4 | AAB52428 | Aab52428 Peptide B |
| 673 | 27 | 27.6 | 14 | 4 | AAB52429 | Aab52429 Peptide B |
| 674 | 27 | 27.6 | 14 | 4 | AAB52244 | Aab52244 Peptide B |
| 675 | 27 | 27.6 | 14 | 8 | ADI66718 | Adi66718 Rat bacte |
| 676 | 27 | 27.6 | 14 | 8 | ADI66719 | Adi66719 Rat bacte |
| 677 | 27 | 27.6 | 14 | 8 | ADI66537 | Adi66537 Rat bacte |
| 678 | 27 | 27.6 | 14 | 8 | ADM91451 | Adm91451 Bacterici |
| 679 | 27 | 27.6 | 14 | 8 | ADM91450 | Adm91450 Bacterici |
| 680 | 27 | 27.6 | 14 | 8 | ADM91349 | Adm91349 Bacterici |
| 681 | 27 | 27.6 | 15 | 1 | AAP70354 | Aap70354 Sequence |
| 682 | 27 | 27.6 | 15 | 4 | AAG64381 | Aag64381 Human act |
| 683 | 27 | 27.6 | 15 | 6 | ABR32250 | Abr32250 Human can |

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|---|---|---|---|---|---|---|
| 684 | 27 | 27.6 | 15 | 6 | ABR31879 | Abr31879 Human can |
| 685 | 27 | 27.6 | 15 | 6 | ABR32222 | Abr32222 Human can |
| 686 | 27 | 27.6 | 15 | 8 | ADV32024 | Adv32024 Human 109 |
| 687 | 27 | 27.6 | 15 | 8 | ADV31996 | Adv31996 Human 109 |
| 688 | 27 | 27.6 | 15 | 9 | AEB12248 | Aeb12248 Cyclin A |
| 689 | 27 | 27.6 | 15 | 9 | AEB12244 | Aeb12244 Cyclin A |
| 690 | 27 | 27.6 | 15 | 9 | AEB12247 | Aeb12247 Cyclin A |
| 691 | 27 | 27.6 | 15 | 9 | AEC70708 | Aec70708 Human 109 |
| 692 | 27 | 27.6 | 15 | 9 | AEC71051 | Aec71051 Human 109 |
| 693 | 27 | 27.6 | 15 | 9 | AEC71079 | Aec71079 Human 109 |
| 694 | 27 | 27.6 | 16 | 2 | AAR64603 | Aar64603 RF-1 pept |
| 695 | 27 | 27.6 | 16 | 2 | AAW59266 | Aaw59266 Myc-tag p |
| 696 | 27 | 27.6 | 16 | 4 | AAB55206 | Aab55206 Anti-RSV |
| 697 | 27 | 27.6 | 16 | 5 | AAE18707 | Aae18707 Major his |
| 698 | 27 | 27.6 | 16 | 8 | ADI41392 | Adi41392 Human HGP |
| 699 | 27 | 27.6 | 17 | 2 | AAW14812 | Aaw14812 sis oncog |
| 700 | 27 | 27.6 | 17 | 2 | AAW14830 | Aaw14830 PDGF-2 on |
| 701 | 27 | 27.6 | 17 | 2 | AAR73655 | Aar73655 PDGF(73-8 |
| 702 | 27 | 27.6 | 17 | 2 | AAR73665 | Aar73665 Cyclic PD |
| 703 | 27 | 27.6 | 17 | 2 | AAR64604 | Aar64604 RF-1 pept |
| 704 | 27 | 27.6 | 17 | 3 | AAY52611 | Aay52611 v-sis enc |
| 705 | 27 | 27.6 | 17 | 4 | AAB55207 | Aab55207 Anti-RSV |
| 706 | 27 | 27.6 | 17 | 5 | AAU82600 | Aau82600 Llama CDR |
| 707 | 27 | 27.6 | 17 | 8 | ADO42136 | Ado42136 Marburg i |
| 708 | 27 | 27.6 | 18 | 2 | AAR22589 | Aar22589 Nonlinear |
| 709 | 27 | 27.6 | 18 | 2 | AAR73656 | Aar73656 PDGF(73-8 |
| 710 | 27 | 27.6 | 18 | 2 | AAR73657 | Aar73657 Ac-PDGF(7 |
| 711 | 27 | 27.6 | 18 | 2 | AAR64605 | Aar64605 RF-1 pept |
| 712 | 27 | 27.6 | 18 | 2 | AAR85995 | Aar85995 Pro-endot |
| 713 | 27 | 27.6 | 18 | 4 | AAB55208 | Aab55208 Anti-RSV |
| 714 | 27 | 27.6 | 18 | 6 | ABU03297 | Abu03297 Human exp |
| 715 | 27 | 27.6 | 18 | 9 | AED68532 | Aed68532 Antimicro |
| 716 | 27 | 27.6 | 18 | 10 | AEF01917 | Aef01917 Ii-key/ H |
| 717 | 27 | 27.6 | 18 | 10 | AEF01959 | Aef01959 Ii-key/ H |
| 718 | 27 | 27.6 | 18 | 10 | AEF01944 | Aef01944 Ii-key/ H |
| 719 | 27 | 27.6 | 19 | 2 | AAR64606 | Aar64606 RF-1 pept |
| 720 | 27 | 27.6 | 19 | 3 | AAY65729 | Aay65729 Breast ca |
| 721 | 27 | 27.6 | 19 | 4 | AAB55209 | Aab55209 Anti-RSV |
| 722 | 27 | 27.6 | 19 | 6 | ABP58053 | Abp58053 Collagen |
| 723 | 27 | 27.6 | 20 | 2 | AAR64607 | Aar64607 RF-1 pept |
| 724 | 27 | 27.6 | 20 | 2 | AAW12307 | Aaw12307 Immunogen |
| 725 | 27 | 27.6 | 20 | 2 | AAW30098 | Aaw30098 Neurotran |
| 726 | 27 | 27.6 | 20 | 2 | AAW62866 | Aaw62866 Epitope o |
| 727 | 27 | 27.6 | 20 | 4 | AAB55210 | Aab55210 Anti-RSV |
| 728 | 27 | 27.6 | 20 | 4 | AAE12829 | Aae12829 Human MHC |
| 729 | 27 | 27.6 | 20 | 6 | ABP55284 | Abp55284 Human mus |
| 730 | 27 | 27.6 | 20 | 8 | ADS17221 | Ads17221 Peptide # |
| 731 | 27 | 27.6 | 20 | 8 | ADS17222 | Ads17222 MHC Class |
| 732 | 27 | 27.6 | 21 | 2 | AAR64608 | Aar64608 RF-1 pept |
| 733 | 27 | 27.6 | 21 | 3 | AAY89352 | Aay89352 Core poly |
| 734 | 27 | 27.6 | 21 | 3 | AAY89225 | Aay89225 Core poly |
| 735 | 27 | 27.6 | 21 | 4 | AAB55211 | Aab55211 Anti-RSV |
| 736 | 27 | 27.6 | 21 | 4 | AAB77578 | Aab77578 Core poly |
| 737 | 27 | 27.6 | 21 | 4 | AAB77753 | Aab77753 Core poly |
| 738 | 27 | 27.6 | 21 | 4 | ABB02059 | Abb02059 Viral cor |
| 739 | 27 | 27.6 | 21 | 4 | ABB02236 | Abb02236 Viral cor |
| 740 | 27 | 27.6 | 21 | 4 | ABB00583 | Abb00583 RSV F1 pr |
| 741 | 27 | 27.6 | 21 | 4 | ABB00760 | Abb00760 Viral DP1 |
| 742 | 27 | 27.6 | 21 | 4 | AAU13131 | Aau13131 DP178-lik |
| 743 | 27 | 27.6 | 21 | 4 | AAU13306 | Aau13306 DP178-lik |
| 744 | 27 | 27.6 | 21 | 5 | ADE02079 | Ade02079 Hybrid po |

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|---|---|---|---|---|---|---|
| 745 | 27 | 27.6 | 21 | 5 | ADE02256 | Ade02256 Hybrid po |
| 746 | 27 | 27.6 | 21 | 7 | ADC17642 | Adc17642 Type IV c |
| 747 | 27 | 27.6 | 21 | 7 | ADF30617 | Adf30617 Rat angio |
| 748 | 27 | 27.6 | 21 | 8 | ADR19164 | Adr19164 Type IV c |
| 749 | 27 | 27.6 | 22 | 2 | AAR48546 | Aar48546 Sequence |
| 750 | 27 | 27.6 | 22 | 2 | AAR64609 | Aar64609 RF-1 pept |
| 751 | 27 | 27.6 | 22 | 2 | AAW47933 | Aaw47933 Antigenic |
| 752 | 27 | 27.6 | 22 | 2 | AAY18824 | Aay18824 Lecithin: |
| 753 | 27 | 27.6 | 22 | 2 | AAY18853 | Aay18853 Lecithin: |
| 754 | 27 | 27.6 | 22 | 2 | AAY18846 | Aay18846 Lecithin: |
| 755 | 27 | 27.6 | 22 | 2 | AAY18856 | Aay18856 Lecithin: |
| 756 | 27 | 27.6 | 22 | 2 | AAY18789 | Aay18789 Lecithin: |
| 757 | 27 | 27.6 | 22 | 2 | AAY18867 | Aay18867 Lecithin: |
| 758 | 27 | 27.6 | 22 | 2 | AAY18825 | Aay18825 Lecithin: |
| 759 | 27 | 27.6 | 22 | 2 | AAY18836 | Aay18836 Lecithin: |
| 760 | 27 | 27.6 | 22 | 2 | AAY18830 | Aay18830 Lecithin: |
| 761 | 27 | 27.6 | 22 | 2 | AAY18828 | Aay18828 Lecithin: |
| 762 | 27 | 27.6 | 22 | 2 | AAY18858 | Aay18858 Lecithin: |
| 763 | 27 | 27.6 | 22 | 2 | AAY18865 | Aay18865 Lecithin: |
| 764 | 27 | 27.6 | 22 | 2 | AAY18854 | Aay18854 Lecithin: |
| 765 | 27 | 27.6 | 22 | 2 | AAY18860 | Aay18860 Lecithin: |
| 766 | 27 | 27.6 | 22 | 2 | AAY18710 | Aay18710 Lecithin: |
| 767 | 27 | 27.6 | 22 | 2 | AAY18759 | Aay18759 Lecithin: |
| 768 | 27 | 27.6 | 22 | 2 | AAY18832 | Aay18832 Lecithin: |
| 769 | 27 | 27.6 | 22 | 2 | AAY18834 | Aay18834 Lecithin: |
| 770 | 27 | 27.6 | 22 | 2 | AAY18829 | Aay18829 Lecithin: |
| 771 | 27 | 27.6 | 22 | 2 | AAY18835 | Aay18835 Lecithin: |
| 772 | 27 | 27.6 | 22 | 2 | AAY18838 | Aay18838 Lecithin: |
| 773 | 27 | 27.6 | 22 | 2 | AAY18823 | Aay18823 Lecithin: |
| 774 | 27 | 27.6 | 22 | 2 | AAY18833 | Aay18833 Lecithin: |
| 775 | 27 | 27.6 | 22 | 2 | AAY18847 | Aay18847 Lecithin: |
| 776 | 27 | 27.6 | 22 | 2 | AAY18868 | Aay18868 Lecithin: |
| 777 | 27 | 27.6 | 22 | 2 | AAY18831 | Aay18831 Lecithin: |
| 778 | 27 | 27.6 | 22 | 2 | AAY18703 | Aay18703 Lecithin: |
| 779 | 27 | 27.6 | 22 | 2 | AAY18772 | Aay18772 Lecithin: |
| 780 | 27 | 27.6 | 22 | 2 | AAY19085 | Aay19085 Lecithin: |
| 781 | 27 | 27.6 | 22 | 2 | AAY19108 | Aay19108 Lecithin: |
| 782 | 27 | 27.6 | 22 | 2 | AAY19121 | Aay19121 Lecithin: |
| 783 | 27 | 27.6 | 22 | 2 | AAY19087 | Aay19087 Lecithin: |
| 784 | 27 | 27.6 | 22 | 2 | AAY19092 | Aay19092 Lecithin: |
| 785 | 27 | 27.6 | 22 | 2 | AAY19101 | Aay19101 Lecithin: |
| 786 | 27 | 27.6 | 22 | 2 | AAY19078 | Aay19078 Lecithin: |
| 787 | 27 | 27.6 | 22 | 2 | AAY19112 | Aay19112 Lecithin: |
| 788 | 27 | 27.6 | 22 | 2 | AAY19119 | Aay19119 Lecithin: |
| 789 | 27 | 27.6 | 22 | 2 | AAY18964 | Aay18964 Lecithin: |
| 790 | 27 | 27.6 | 22 | 2 | AAY19084 | Aay19084 Lecithin: |
| 791 | 27 | 27.6 | 22 | 2 | AAY19107 | Aay19107 Lecithin: |
| 792 | 27 | 27.6 | 22 | 2 | AAY19026 | Aay19026 Lecithin: |
| 793 | 27 | 27.6 | 22 | 2 | AAY19090 | Aay19090 Lecithin: |
| 794 | 27 | 27.6 | 22 | 2 | AAY18957 | Aay18957 Lecithin: |
| 795 | 27 | 27.6 | 22 | 2 | AAY19079 | Aay19079 Lecithin: |
| 796 | 27 | 27.6 | 22 | 2 | AAY19086 | Aay19086 Lecithin: |
| 797 | 27 | 27.6 | 22 | 2 | AAY19110 | Aay19110 Lecithin: |
| 798 | 27 | 27.6 | 22 | 2 | AAY19122 | Aay19122 Lecithin: |
| 799 | 27 | 27.6 | 22 | 2 | AAY19043 | Aay19043 Lecithin: |
| 800 | 27 | 27.6 | 22 | 2 | AAY19077 | Aay19077 Lecithin: |
| 801 | 27 | 27.6 | 22 | 2 | AAY19083 | Aay19083 Lecithin: |
| 802 | 27 | 27.6 | 22 | 2 | AAY19114 | Aay19114 Lecithin: |
| 803 | 27 | 27.6 | 22 | 2 | AAY19089 | Aay19089 Lecithin: |
| 804 | 27 | 27.6 | 22 | 2 | AAY19013 | Aay19013 Lecithin: |
| 805 | 27 | 27.6 | 22 | 2 | AAY19082 | Aay19082 Lecithin: |

| | | | | | | |
|---|---|---|---|---|---|---|
| 806 | 27 | 27.6 | 22 | 2 | AAY19088 | Aay19088 Lecithin: |
| 807 | 27 | 27.6 | 22 | 2 | AAY19100 | Aay19100 Lecithin: |
| 808 | 27 | 27.6 | 22 | 2 | AAY19376 | Aay19376 Lecithin: |
| 809 | 27 | 27.6 | 22 | 2 | AAY19211 | Aay19211 Lecithin: |
| 810 | 27 | 27.6 | 22 | 2 | AAY19267 | Aay19267 Lecithin: |
| 811 | 27 | 27.6 | 22 | 2 | AAY19355 | Aay19355 Lecithin: |
| 812 | 27 | 27.6 | 22 | 2 | AAY19361 | Aay19361 Lecithin: |
| 813 | 27 | 27.6 | 22 | 2 | AAY19373 | Aay19373 Lecithin: |
| 814 | 27 | 27.6 | 22 | 2 | AAY19338 | Aay19338 Lecithin: |
| 815 | 27 | 27.6 | 22 | 2 | AAY19332 | Aay19332 Lecithin: |
| 816 | 27 | 27.6 | 22 | 2 | AAY19346 | Aay19346 Lecithin: |
| 817 | 27 | 27.6 | 22 | 2 | AAY19364 | Aay19364 Lecithin: |
| 818 | 27 | 27.6 | 22 | 2 | AAY19331 | Aay19331 Lecithin: |
| 819 | 27 | 27.6 | 22 | 2 | AAY19339 | Aay19339 Lecithin: |
| 820 | 27 | 27.6 | 22 | 2 | AAY19354 | Aay19354 Lecithin: |
| 821 | 27 | 27.6 | 22 | 2 | AAY19218 | Aay19218 Lecithin: |
| 822 | 27 | 27.6 | 22 | 2 | AAY19337 | Aay19337 Lecithin: |
| 823 | 27 | 27.6 | 22 | 2 | AAY19342 | Aay19342 Lecithin: |
| 824 | 27 | 27.6 | 22 | 2 | AAY19297 | Aay19297 Lecithin: |
| 825 | 27 | 27.6 | 22 | 2 | AAY19362 | Aay19362 Lecithin: |
| 826 | 27 | 27.6 | 22 | 2 | AAY19340 | Aay19340 Lecithin: |
| 827 | 27 | 27.6 | 22 | 2 | AAY19366 | Aay19366 Lecithin: |
| 828 | 27 | 27.6 | 22 | 2 | AAY19343 | Aay19343 Lecithin: |
| 829 | 27 | 27.6 | 22 | 2 | AAY19344 | Aay19344 Lecithin: |
| 830 | 27 | 27.6 | 22 | 2 | AAY19375 | Aay19375 Lecithin: |
| 831 | 27 | 27.6 | 22 | 2 | AAY19333 | Aay19333 Lecithin: |
| 832 | 27 | 27.6 | 22 | 2 | AAY19280 | Aay19280 Lecithin: |
| 833 | 27 | 27.6 | 22 | 2 | AAY19336 | Aay19336 Lecithin: |
| 834 | 27 | 27.6 | 22 | 2 | AAY19341 | Aay19341 Lecithin: |
| 835 | 27 | 27.6 | 22 | 2 | AAY19368 | Aay19368 Lecithin: |
| 836 | 27 | 27.6 | 22 | 2 | AAY18565 | Aay18565 Lecithin: |
| 837 | 27 | 27.6 | 22 | 2 | AAY18569 | Aay18569 Lecithin: |
| 838 | 27 | 27.6 | 22 | 2 | AAY18597 | Aay18597 Lecithin: |
| 839 | 27 | 27.6 | 22 | 2 | AAY18496 | Aay18496 Lecithin: |
| 840 | 27 | 27.6 | 22 | 2 | AAY18567 | Aay18567 Lecithin: |
| 841 | 27 | 27.6 | 22 | 2 | AAY18583 | Aay18583 Lecithin: |
| 842 | 27 | 27.6 | 22 | 2 | AAY18561 | Aay18561 Lecithin: |
| 843 | 27 | 27.6 | 22 | 2 | AAY18571 | Aay18571 Lecithin: |
| 844 | 27 | 27.6 | 22 | 2 | AAY18590 | Aay18590 Lecithin: |
| 845 | 27 | 27.6 | 22 | 2 | AAY18568 | Aay18568 Lecithin: |
| 846 | 27 | 27.6 | 22 | 2 | AAY18509 | Aay18509 Lecithin: |
| 847 | 27 | 27.6 | 22 | 2 | AAY18572 | Aay18572 Lecithin: |
| 848 | 27 | 27.6 | 22 | 2 | AAY18560 | Aay18560 Lecithin: |
| 849 | 27 | 27.6 | 22 | 2 | AAY18526 | Aay18526 Lecithin: |
| 850 | 27 | 27.6 | 22 | 2 | AAY18575 | Aay18575 Lecithin: |
| 851 | 27 | 27.6 | 22 | 2 | AAY18604 | Aay18604 Lecithin: |
| 852 | 27 | 27.6 | 22 | 2 | AAY18591 | Aay18591 Lecithin: |
| 853 | 27 | 27.6 | 22 | 2 | AAY18605 | Aay18605 Lecithin: |
| 854 | 27 | 27.6 | 22 | 2 | AAY18562 | Aay18562 Lecithin: |
| 855 | 27 | 27.6 | 22 | 2 | AAY18570 | Aay18570 Lecithin: |
| 856 | 27 | 27.6 | 22 | 2 | AAY18573 | Aay18573 Lecithin: |
| 857 | 27 | 27.6 | 22 | 2 | AAY18440 | Aay18440 Lecithin: |
| 858 | 27 | 27.6 | 22 | 2 | AAY18566 | Aay18566 Lecithin: |
| 859 | 27 | 27.6 | 22 | 2 | AAY18593 | Aay18593 Lecithin: |
| 860 | 27 | 27.6 | 22 | 2 | AAY18595 | Aay18595 Lecithin: |
| 861 | 27 | 27.6 | 22 | 2 | AAY18602 | Aay18602 Lecithin: |
| 862 | 27 | 27.6 | 22 | 2 | AAY18447 | Aay18447 Lecithin: |
| 863 | 27 | 27.6 | 22 | 2 | AAY18584 | Aay18584 Lecithin: |
| 864 | 27 | 27.6 | 22 | 4 | AAB55212 | Aab55212 Anti-RSV |
| 865 | 27 | 27.6 | 22 | 7 | ADD88522 | Add88522 Influenza |
| 866 | 27 | 27.6 | 22 | 7 | ADG18287 | Adg18287 Influenza |

| | | | | | | |
|---|---|---|---|---|---|---|
| 867 | 27 | 27.6 | 22 | 8 | ADG21051 | Adg21051 Apolipopr |
| 868 | 27 | 27.6 | 22 | 8 | ADG21071 | Adg21071 Apolipopr |
| 869 | 27 | 27.6 | 22 | 8 | ADG21041 | Adg21041 Apolipopr |
| 870 | 27 | 27.6 | 22 | 8 | ADG21042 | Adg21042 Apolipopr |
| 871 | 27 | 27.6 | 22 | 8 | ADG21064 | Adg21064 Apolipopr |
| 872 | 27 | 27.6 | 22 | 8 | ADG21006 | Adg21006 Apolipopr |
| 873 | 27 | 27.6 | 22 | 8 | ADG21040 | Adg21040 Apolipopr |
| 874 | 27 | 27.6 | 22 | 8 | ADG21050 | Adg21050 Apolipopr |
| 875 | 27 | 27.6 | 22 | 8 | ADG21045 | Adg21045 Apolipopr |
| 876 | 27 | 27.6 | 22 | 8 | ADG21053 | Adg21053 Apolipopr |
| 877 | 27 | 27.6 | 22 | 8 | ADG20927 | Adg20927 Apolipopr |
| 878 | 27 | 27.6 | 22 | 8 | ADG21052 | Adg21052 Apolipopr |
| 879 | 27 | 27.6 | 22 | 8 | ADG20920 | Adg20920 Apolipopr |
| 880 | 27 | 27.6 | 22 | 8 | ADG20989 | Adg20989 Apolipopr |
| 881 | 27 | 27.6 | 22 | 8 | ADG21055 | Adg21055 Apolipopr |
| 882 | 27 | 27.6 | 22 | 8 | ADG21063 | Adg21063 Apolipopr |
| 883 | 27 | 27.6 | 22 | 8 | ADG21073 | Adg21073 Apolipopr |
| 884 | 27 | 27.6 | 22 | 8 | ADG21075 | Adg21075 Apolipopr |
| 885 | 27 | 27.6 | 22 | 8 | ADG21046 | Adg21046 Apolipopr |
| 886 | 27 | 27.6 | 22 | 8 | ADG21049 | Adg21049 Apolipopr |
| 887 | 27 | 27.6 | 22 | 8 | ADG21084 | Adg21084 Apolipopr |
| 888 | 27 | 27.6 | 22 | 8 | ADG21048 | Adg21048 Apolipopr |
| 889 | 27 | 27.6 | 22 | 8 | ADG21077 | Adg21077 Apolipopr |
| 890 | 27 | 27.6 | 22 | 8 | ADG21085 | Adg21085 Apolipopr |
| 891 | 27 | 27.6 | 22 | 8 | ADG20976 | Adg20976 Apolipopr |
| 892 | 27 | 27.6 | 22 | 8 | ADG21047 | Adg21047 Apolipopr |
| 893 | 27 | 27.6 | 22 | 8 | ADG21070 | Adg21070 Apolipopr |
| 894 | 27 | 27.6 | 22 | 8 | ADG21082 | Adg21082 Apolipopr |
| 895 | 27 | 27.6 | 22 | 8 | ADJ33027 | Adj33027 Apo lipop |
| 896 | 27 | 27.6 | 22 | 8 | ADJ32990 | Adj32990 Apo lipop |
| 897 | 27 | 27.6 | 22 | 8 | ADJ33017 | Adj33017 Apo lipop |
| 898 | 27 | 27.6 | 22 | 8 | ADJ32918 | Adj32918 Apo lipop |
| 899 | 27 | 27.6 | 22 | 8 | ADJ32869 | Adj32869 Apo lipop |
| 900 | 27 | 27.6 | 22 | 8 | ADJ32982 | Adj32982 Apo lipop |
| 901 | 27 | 27.6 | 22 | 8 | ADJ32862 | Adj32862 Apo lipop |
| 902 | 27 | 27.6 | 22 | 8 | ADJ32931 | Adj32931 Apo lipop |
| 903 | 27 | 27.6 | 22 | 8 | ADJ33015 | Adj33015 Apo lipop |
| 904 | 27 | 27.6 | 22 | 8 | ADJ32983 | Adj32983 Apo lipop |
| 905 | 27 | 27.6 | 22 | 8 | ADJ33013 | Adj33013 Apo lipop |
| 906 | 27 | 27.6 | 22 | 8 | ADJ33026 | Adj33026 Apo lipop |
| 907 | 27 | 27.6 | 22 | 8 | ADJ32948 | Adj32948 Apo lipop |
| 908 | 27 | 27.6 | 22 | 8 | ADJ32984 | Adj32984 Apo lipop |
| 909 | 27 | 27.6 | 22 | 8 | ADJ32989 | Adj32989 Apo lipop |
| 910 | 27 | 27.6 | 22 | 8 | ADJ32993 | Adj32993 Apo lipop |
| 911 | 27 | 27.6 | 22 | 8 | ADJ32992 | Adj32992 Apo lipop |
| 912 | 27 | 27.6 | 22 | 8 | ADJ32995 | Adj32995 Apo lipop |
| 913 | 27 | 27.6 | 22 | 8 | ADJ32988 | Adj32988 Apo lipop |
| 914 | 27 | 27.6 | 22 | 8 | ADJ32994 | Adj32994 Apo lipop |
| 915 | 27 | 27.6 | 22 | 8 | ADJ33019 | Adj33019 Apo lipop |
| 916 | 27 | 27.6 | 22 | 8 | ADJ33006 | Adj33006 Apo lipop |
| 917 | 27 | 27.6 | 22 | 8 | ADJ32991 | Adj32991 Apo lipop |
| 918 | 27 | 27.6 | 22 | 8 | ADJ33024 | Adj33024 Apo lipop |
| 919 | 27 | 27.6 | 22 | 8 | ADJ32987 | Adj32987 Apo lipop |
| 920 | 27 | 27.6 | 22 | 8 | ADJ32997 | Adj32997 Apo lipop |
| 921 | 27 | 27.6 | 22 | 8 | ADJ33005 | Adj33005 Apo lipop |
| 922 | 27 | 27.6 | 22 | 8 | ADJ33012 | Adj33012 Apo lipop |
| 923 | 27 | 27.6 | 22 | 9 | ADW92449 | Adw92449 H1N1 infl |
| 924 | 27 | 27.6 | 23 | 2 | AAR64610 | Aar64610 RF-1 pept |
| 925 | 27 | 27.6 | 23 | 2 | AAY07215 | Aay07215 Peptide t |
| 926 | 27 | 27.6 | 23 | 3 | AAY89232 | Aay89232 Core poly |
| 927 | 27 | 27.6 | 23 | 3 | AAY89499 | Aay89499 Core poly |

| | | | | | | |
|---|---|---|---|---|---|---|
| 928 | 27 | 27.6 | 23 | 4 | AAB55213 | Aab55213 Anti-RSV |
| 929 | 27 | 27.6 | 23 | 4 | AAB77585 | Aab77585 Core poly |
| 930 | 27 | 27.6 | 23 | 4 | AAB77900 | Aab77900 Core poly |
| 931 | 27 | 27.6 | 23 | 4 | AAB77901 | Aab77901 Core poly |
| 932 | 27 | 27.6 | 23 | 4 | ABB00908 | Abb00908 Viral DP1 |
| 933 | 27 | 27.6 | 23 | 4 | ABB02374 | Abb02374 Viral cor |
| 934 | 27 | 27.6 | 23 | 4 | ABB02375 | Abb02375 Viral cor |
| 935 | 27 | 27.6 | 23 | 4 | ABB00907 | Abb00907 Viral DP1 |
| 936 | 27 | 27.6 | 23 | 4 | ABB00590 | Abb00590 RSV F1 pr |
| 937 | 27 | 27.6 | 23 | 4 | ABB02066 | Abb02066 Viral cor |
| 938 | 27 | 27.6 | 23 | 4 | AAU13138 | Aau13138 DP178-lik |
| 939 | 27 | 27.6 | 23 | 4 | AAU13453 | Aau13453 DP178-lik |
| 940 | 27 | 27.6 | 23 | 5 | ADE02394 | Ade02394 Hybrid po |
| 941 | 27 | 27.6 | 23 | 5 | ADE02086 | Ade02086 Hybrid po |
| 942 | 27 | 27.6 | 23 | 5 | ADE02395 | Ade02395 Hybrid po |
| 943 | 27 | 27.6 | 23 | 10 | AEF20484 | Aef20484 Human ost |
| 944 | 27 | 27.6 | 24 | 2 | AAR64611 | Aar64611 RF-1 pept |
| 945 | 27 | 27.6 | 24 | 2 | AAW33941 | Aaw33941 Beta1-adr |
| 946 | 27 | 27.6 | 24 | 3 | AAY89500 | Aay89500 Core poly |
| 947 | 27 | 27.6 | 24 | 4 | AAB55214 | Aab55214 Anti-RSV |
| 948 | 27 | 27.6 | 24 | 4 | AAM86218 | Aam86218 Human imm |
| 949 | 27 | 27.6 | 24 | 4 | AAB70120 | Aab70120 Penicilli |
| 950 | 27 | 27.6 | 24 | 4 | AAU13454 | Aau13454 DP178-lik |
| 951 | 27 | 27.6 | 25 | 2 | AAR64612 | Aar64612 RF-1 pept |
| 952 | 27 | 27.6 | 25 | 2 | AAW30494 | Aaw30494 Flea sali |
| 953 | 27 | 27.6 | 25 | 3 | AAY89231 | Aay89231 Core poly |
| 954 | 27 | 27.6 | 25 | 3 | AAY89237 | Aay89237 Core poly |
| 955 | 27 | 27.6 | 25 | 4 | AAB55215 | Aab55215 Anti-RSV |
| 956 | 27 | 27.6 | 25 | 4 | ABB40984 | Abb40984 Peptide # |
| 957 | 27 | 27.6 | 25 | 4 | ABB43082 | Abb43082 Peptide # |
| 958 | 27 | 27.6 | 25 | 4 | AAM34759 | Aam34759 Peptide # |
| 959 | 27 | 27.6 | 25 | 4 | AAM36907 | Aam36907 Peptide # |
| 960 | 27 | 27.6 | 25 | 4 | AAB77590 | Aab77590 Core poly |
| 961 | 27 | 27.6 | 25 | 4 | AAB77584 | Aab77584 Core poly |
| 962 | 27 | 27.6 | 25 | 4 | AAM76801 | Aam76801 Human bon |
| 963 | 27 | 27.6 | 25 | 4 | AAM63981 | Aam63981 Human bra |
| 964 | 27 | 27.6 | 25 | 4 | AAM61844 | Aam61844 Human bra |
| 965 | 27 | 27.6 | 25 | 4 | ABG58482 | Abg58482 Human liv |
| 966 | 27 | 27.6 | 25 | 4 | ABB00595 | Abb00595 RSV F1 pr |
| 967 | 27 | 27.6 | 25 | 4 | ABB02071 | Abb02071 Viral cor |
| 968 | 27 | 27.6 | 25 | 4 | ABB02065 | Abb02065 Viral cor |
| 969 | 27 | 27.6 | 25 | 4 | ABB00589 | Abb00589 RSV F1 pr |
| 970 | 27 | 27.6 | 25 | 4 | AAU13143 | Aau13143 DP178-lik |
| 971 | 27 | 27.6 | 25 | 4 | AAU13137 | Aau13137 DP178-lik |
| 972 | 27 | 27.6 | 25 | 5 | ADE02085 | Ade02085 Hybrid po |
| 973 | 27 | 27.6 | 25 | 5 | ADE02091 | Ade02091 Hybrid po |
| 974 | 27 | 27.6 | 25 | 7 | ADC26852 | Adc26852 B. burgdo |
| 975 | 27 | 27.6 | 25 | 9 | ADV57496 | Adv57496 G protein |
| 976 | 27 | 27.6 | 25 | 9 | ADV55203 | Adv55203 G protein |
| 977 | 27 | 27.6 | 25 | 9 | ADV56698 | Adv56698 G protein |
| 978 | 27 | 27.6 | 25 | 9 | ADV55545 | Adv55545 G protein |
| 979 | 27 | 27.6 | 25 | 9 | ADZ38618 | Adz38618 Group A S |
| 980 | 27 | 27.6 | 26 | 2 | AAR64613 | Aar64613 RF-1 pept |
| 981 | 27 | 27.6 | 26 | 4 | AAB55216 | Aab55216 Anti-RSV |
| 982 | 27 | 27.6 | 26 | 10 | AEE38856 | Aee38856 Human ser |
| 983 | 27 | 27.6 | 27 | 2 | AAR50607 | Aar50607 G-protein |
| 984 | 27 | 27.6 | 27 | 2 | AAR64614 | Aar64614 RF-1 pept |
| 985 | 27 | 27.6 | 27 | 2 | AAW02799 | Aaw02799 G-protein |
| 986 | 27 | 27.6 | 27 | 2 | AAW82353 | Aaw82353 Flea sali |
| 987 | 27 | 27.6 | 27 | 3 | AAY89236 | Aay89236 Core poly |
| 988 | 27 | 27.6 | 27 | 3 | AAY89230 | Aay89230 Core poly |

RESULT 4
ADZ69803
ID  ADZ69803 standard; peptide; 9 AA.
XX
AC  ADZ69803;
XX
DT  28-JUL-2005  (first entry)
XX
DE  Botulinum toxin type A peptide SEQ ID NO:78.
XX
KW  toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW  autonomic nervous system disease; pain; neuromuscular disease;
KW  cervical dystonia; migraine.
XX
OS  Clostridium botulinum.
XX
PN  US2005106182-A1.
XX
PD  19-MAY-2005.
XX
PF  17-NOV-2003; 2003US-00715810.
XX
PR  17-NOV-2003; 2003US-00715810.
XX
PA  (LISS/) LI S.
PA  (AOKI/) AOKI K R.
XX
PI  Li S,  Aoki KR;
XX
DR  WPI; 2005-365766/37.
XX
PT  Treating botulinum toxin intoxication in a mammal, comprises
PT  administering a rescue agent comprising an inactive botulinum toxin and a
PT  modified nontoxic nonhemagglutinin to a mammal.
XX
PS  Disclosure; SEQ ID NO 78; 61pp; English.
XX
CC  The invention relates to a method (M1) for treating botulinum toxin
CC  intoxication in a mammal. (M1) comprises administering at least one
CC  rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC  being glycosylated, having reduced antigenicity, and being inactive; (2)
CC  making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC  in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC  comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC  non-Clostridium botulinum cell (III) comprising a vector operatively
CC  harboring a nucleotide sequence encoding a single chain botulinum toxin
CC  and a vector operatively harboring nucleotide sequence encoding a
CC  nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC  condition, an autonomic nervous system disorder and/or pain, which
CC  involves administering (II) to the mammal in need of the toxins. (II) is
CC  also useful for the treatment of neuromuscular disorders, cervical
CC  dystonia and migraine. The present sequence represents a Clostridium
CC  botulinum toxin type A peptide sequence, which is used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 9 AA;

  Query Match             43.9%;  Score 43;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          7 VNTQIDLIR 15
              |||||||||
Db          1 VNTQIDLIR 9
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715-733

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RESULT 3
ADY20753
ID   ADY20753 standard; peptide; 12 AA.
XX
AC   ADY20753;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Botulinum peptide fragment #1.
XX
KW   Delivery mechanism; toxin; endocytosis; bacterial infection;
KW   viral infection; antibacterial; virucide.
XX
OS   Unidentified.
XX
PN   WO2005014798-A2.
XX
PD   17-FEB-2005.
XX
PF   31-MAR-2004; 2004WO-US009829.
XX
PR   31-MAR-2003; 2003US-0459185P.
XX
PA   (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI   Murphy JR,  Ratts R,  Pearson DA;
XX
DR   WPI; 2005-173098/18.
XX
PT   New compound, useful in the manufacture of a medicament for inhibiting
PT   cell death or the translocation of a viral or bacterial toxin or viral
PT   transcription factor for treating or preventing bacterial or viral
PT   infections.
XX
PS   Disclosure; Fig 9; 100pp; English.
XX
CC   The invention relates to a new peptide compound and a nucleic acid
CC   sequence encoding the peptide. The invention also relates to a method of
CC   identifying a compound that inhibits cell death in a mammal and a method
CC   of identifying a compound that promotes cell death in a mammal. The
CC   compound is useful in the manufacture of a medicament for inhibiting cell
CC   death in a mammal. The compound inhibits the translocation of a viral or
CC   bacterial toxin from the lumen of an endosome to the cytosol of the cell
CC   or the translocation of a viral or retroviral transcription factor. The
CC   compound is further reacted with a monoclonal antibody, or its fragment
CC   to form a covalent bond between a sulfur atom of the antibody and the
CC   maleimide group of the compound. Identifying a compound that inhibits
CC   cell death in a mammal comprises isolating endosomes from the cell,
CC   placing the endosomes in a cytosolic buffer, contacting the endosomes
CC   with a fusion protein-toxin, where the protein comprises a binding moiety
CC   for a component of the cell membrane of the cell and the toxin comprises
CC   a fragment of Diphtheria toxin, contacting the endosomes with a cytosolic
CC   translocation factor complex, contacting the endosomes with the compound
CC   and measuring translocation of the toxin, where a decreased level of the
CC   translocation relative to that observed in the absence of the compound
CC   indicates that the compound inhibits the cell death. Identifying a
CC   compound that promotes cell death in a mammal comprises isolating
CC   endosomes from the cell, placing the endosomes in a cytosolic buffer,
CC   contacting the endosomes with a fusion protein-toxin, where the protein
CC   comprises a binding moiety for a component of the cell membrane of the
CC   cell and the toxin comprises a fragment of Diphtheria toxin, contacting
```

CC the endosomes with a cytosolic translocation factor complex, contacting
CC the endosomes with the compound and measuring translocation of the toxin,
CC where an increased level of the translocation relative to that observed
CC in the absence of the compound indicates that the compound promotes the
CC cell death. The compound is useful in the manufacture of a medicament for
CC inhibiting cell death in a mammal or for inhibiting the translocation of
CC a viral or bacterial toxin, e.g., Diphtheria toxin, a Botulinum toxin,
CC Anthrax toxin LF or Anthrax toxin EF from the lumen of an endosome to the
CC cytosol of the cell or the translocation of a viral or retroviral
CC transcription factor, e.g., human immunodeficiency virus reverse
CC transcriptase or Tat for treating or preventing bacterial or viral
CC infections. This sequence represents a botulinum peptide fragment used in
CC the scope of the invention.
XX
SQ Sequence 12 AA;

Query Match 53.1%; Score 52; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 AKVNTQIDLIR 15
              ||||||||||
Db          1 AKVNTQIDLIR 11
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RESULT 47
ABP68020
ID  ABP68020 standard; peptide; 12 AA.
XX
AC  ABP68020;
XX
DT  08-JAN-2003  (first entry)
XX
DE  Bacillus thuringiensis toxin Cry related peptide #13.
XX
KW  Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW  pepsin; PCS.
XX
OS  Bacillus thuringiensis.
OS  Synthetic.
XX
PN  FR2822157-A1.
XX
PD  20-SEP-2002.
XX
PF  19-MAR-2001; 2001FR-00003691.
XX
PR  19-MAR-2001; 2001FR-00003691.
XX
PA  (AVET ) AVENTIS CROPSCIENCE SA.
XX
PI  Freyssinet G,  Rang C,  Frutos R;
XX
DR  WPI; 2003-002439/01.
XX
PT  New modified Cry protein, useful as insecticide, comprises at least one
PT  additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS  Example 2; Page 21; 134pp; French.
XX
CC  The present invention describes a modified Cry protein (I) that is
CC  sensitive to pepsin and comprises at least one additional pepsin cleavage
CC  site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC  proteins by incorporating at least one extra PCS; (b) polynucleotides
CC  (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC  (II) and terminator; (d) expression or transformation vector (III) that
CC  contains CG; (e) host organism (IV) transformed with (III), also, where
CC  the organism is a plant, its parts and seeds; (f) production of (I) by
CC  growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC  against (I). (I) has insecticide activity. (I) can be used as
CC  insecticides, particularly where expressed in transgenic plants. (I) are
CC  sensitive to enzymes in the digestive tract of mammals, so do not persist
CC  in the tract (lack of persistence is required by regulatory authorities
CC  for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC  increase degradation in the digestive tract of insects, so have no effect
CC  on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC  represent sequences used in the exemplification of the present invention
XX
SQ  Sequence 12 AA;

715-733

Query Match  33.7%;  Score 33;  DB 6;  Length 12;
Best Local Similarity  71.4%;  Pred. No. 1.8e+02;
Matches  5;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  2 NWLAKVN 8
      ||||::|

Db 2 NWLAELN 8

dem93
673-691

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RESULT 48
US-10-506-877-32
; Sequence 32, Application US/10506877
; Publication No. US20060148093A1
; GENERAL INFORMATION:
;  APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
;  TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MODIFIED PROTEINS
;  FILE REFERENCE: 56954 PCT (70207)
;  CURRENT APPLICATION NUMBER: US/10/506,877
;  CURRENT FILING DATE:  2004-09-03
;  PRIOR APPLICATION NUMBER: 60/363,179
;  PRIOR FILING DATE: 2002-03-11
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphopeptide sequence
US-10-506-877-32

  Query Match             27.5%;  Score 25;  DB 6;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 9.2e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 VSYIAN 15
                :||:||
Db          7 LSYVAN 12
```

# SCORE Search Results Details for Application 10821669 and Search Result us-10-821-669-1_copy_715_733.szlm30.rag.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10821669 and Search Result us-10-821-669-1_copy_715_733.szlm30.rag.

start

Go Back to previous page

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                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          November  1, 2006, 12:48:32 ; Search time 92.5641 Seconds
                                             (without alignments)
                                             93.850 Million cell updates/sec

Title:           US-10-821-669-1_COPY_715_733
Perfect score:   98
Sequence:        1 TNWLAKVNTQIDLIRKKMK 19

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :        A_Geneseq_8:*
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                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
                 9:  geneseqp2005s:*
                 10:  geneseqp2006s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
```

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 98 | 100.0 | 19 | 9 | ADW11060 | Adw11060 Clostridi |
| 2 | 98 | 100.0 | 27 | 9 | ADW11113 | Adw11113 Clostridi |
| 3 | 52 | 53.1 | 12 | 9 | ADY20753 | Ady20753 Botulinum |
| 4 | 43 | 43.9 | 9 | 9 | ADZ69803 | Adz69803 Botulinum |
| 5 | 38.5 | 39.3 | 22 | 2 | AAY18841 | Aay18841 Lecithin: |
| 6 | 38.5 | 39.3 | 22 | 2 | AAY19095 | Aay19095 Lecithin: |
| 7 | 38.5 | 39.3 | 22 | 2 | AAY19349 | Aay19349 Lecithin: |
| 8 | 38.5 | 39.3 | 22 | 2 | AAY18578 | Aay18578 Lecithin: |
| 9 | 38.5 | 39.3 | 22 | 8 | ADG21058 | Adg21058 Apolipopr |
| 10 | 38.5 | 39.3 | 22 | 8 | ADJ33000 | Adj33000 Apo lipop |
| 11 | 38 | 38.8 | 22 | 2 | AAY18741 | Aay18741 Lecithin: |
| 12 | 38 | 38.8 | 22 | 2 | AAY18995 | Aay18995 Lecithin: |
| 13 | 38 | 38.8 | 22 | 2 | AAY19249 | Aay19249 Lecithin: |
| 14 | 38 | 38.8 | 22 | 2 | AAY18478 | Aay18478 Lecithin: |
| 15 | 38 | 38.8 | 22 | 8 | ADG20958 | Adg20958 Apolipopr |
| 16 | 38 | 38.8 | 22 | 8 | ADJ32900 | Adj32900 Apo lipop |
| 17 | 36 | 36.7 | 22 | 2 | AAR48545 | Aar48545 Sequence |
| 18 | 36 | 36.7 | 22 | 9 | AEB28559 | Aeb28559 Human apo |
| 19 | 36 | 36.7 | 22 | 9 | AEB11518 | Aeb11518 Apolipopr |
| 20 | 35 | 35.7 | 9 | 9 | ADZ69802 | Adz69802 Botulinum |

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 13:29:52 ; Search time 19 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-10-821-669-1_COPY_715_733
Perfect score: 98
Sequence: 1 TNWLAKVNTQIDLIRKKMK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 331034

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

715-733

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RESULT 1
US-10-715-810-78
; Sequence 78, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 721-729)
US-10-715-810-78

  Query Match           43.9%;  Score 43;  DB 5;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 VNTQIDLIR 15
              |||||||||
Db          1 VNTQIDLIR 9
```

715-733

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RESULT 25
US-10-946-371-30
; Sequence 30, Application US/10946371
; Publication No. US20050208587A1
; GENERAL INFORMATION:
;  APPLICANT: CARDOSO, ROSA
;  APPLICANT:  WILSON, IAN
;  APPLICANT:  BURTON, DENNIS
;  APPLICANT:  DAWSON, PHILIP
;  TITLE OF INVENTION: PEPTIDES THAT BIND TO BROADLY NEUTRALIZING ANTI-HIV
;  TITLE OF INVENTION:  ANTIBODY-STRUCTURE OF 4E10 FAB FRAGMENT COMPLEX, USES
;  TITLE OF INVENTION:  THEREOF, COMPOSITIONS THEREFROM
;  FILE REFERENCE: 678501-2001.1
;  CURRENT APPLICATION NUMBER: US/10/946,371
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: 60/504,123
;  PRIOR FILING DATE: 2003-09-19
;  PRIOR APPLICATION NUMBER: PCT/EP02/10070
;  PRIOR FILING DATE: 2002-09-09
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 30
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-946-371-30

  Query Match             35.7%;  Score 35;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          6 TNWLAK 11
```

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RESULT 24
US-10-715-810-77
; Sequence 77, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 712-720)
US-10-715-810-77

  Query Match           35.7%;  Score 35;  DB 5;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          4 TNWLAK 9
```

```
RESULT 22
ADY81603
ID   ADY81603 standard; peptide; 15 AA.
XX
AC   ADY81603;
XX
DT   16-JUN-2005  (first entry)
XX
DE   HIV-1 antibody 4E10 binding peptide #21.
XX
KW   diagnosis; pharmaceutical; immunogenicity; immunostimulant; anti-HIV;
KW   vaccine.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO2005028499-A2.
XX
PD   31-MAR-2005.
XX
PF   20-SEP-2004; 2004WO-US030747.
XX
PR   19-SEP-2003; 2003US-0504123P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Cardoso R,  Wilson I,  Burton D,  Dawson P;
XX
DR   WPI; 2005-254114/26.
XX
PT   New Fab 4E10:KGND complex having an X-ray diffraction pattern, useful for
PT   eliciting antibodies or in a diagnostic, pharmaceutical immunogenic,
PT   immunological or vaccine composition.
XX
PS   Claim 46; Page 115; 190pp; English.
XX
CC   The invention relates to a Fab 4E10:KGND complex having an X-ray
CC   diffraction pattern corresponding to or resulting from any or all of
CC   those given in the specification and having the structure defined by the
CC   coordinates listed in the specification. The complex is useful for
CC   eliciting antibodies or in a diagnostic, pharmaceutical immunogenic,
CC   immunological or vaccine composition. The present sequence represents the
CC   HIV-1 antibody 4E10 binding peptide.
XX
SQ   Sequence 15 AA;

  Query Match             35.7%;  Score 35;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          7 TNWLAK 12
```

```
RESULT 20
US-11-416-262-10
; Sequence 10, Application US/11416262
; Publication No. US20060191547A1
; GENERAL INFORMATION:
;  APPLICANT: Conkling, Mark
;  TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
;  TITLE OF INVENTION:  LEVELS IN TOBACCO
;  FILE REFERENCE: VTOB.033C2C
;  CURRENT APPLICATION NUMBER: US/11/416,262
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: 11/077,752
;  PRIOR FILING DATE: 2005-03-10
;  PRIOR APPLICATION NUMBER: 10/729,121
;  PRIOR FILING DATE: 2003-12-05
;  PRIOR APPLICATION NUMBER: 60/297,154
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: PCTUS02/18040
;  PRIOR FILING DATE: 2002-06-06
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-11-416-262-10

  Query Match             28.6%;  Score 28;  DB 7;  Length 26;
  Best Local Similarity   66.7%;  Pred. No. 4.7e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||::
Db         18 TNWLSE 23
```

```
RESULT 23
US-11-439-071-36
; Sequence 36, Application US/11439071
; Publication No. US20060204492A1
;  GENERAL INFORMATION:
;    APPLICANT:  Huse, William D.
;    APPLICANT:  Glaser, Scott M.
;    TITLE OF INVENTION:  Anti-Alpha V Beta 3 Recombinant Human
;    TITLE OF INVENTION:  Antibodies, Nucleic Acids Encoding Same and Methods of Use
;    NUMBER OF SEQUENCES:  100
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/439,071
;      FILING DATE:  22-MAY-2006
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/016,061
;      FILING DATE:  30-JAN-1998
;      APPLICATION NUMBER:  US 08/791,391
;      FILING DATE:  30-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-IX 2965
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-11-439-071-36

  Query Match             27.6%;  Score 27;  DB 7;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 2.3e+02;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WLAKVNT 9
              |:|||::
Db          1 WVAKVSS 7
```

```
RESULT 29
US-11-434-137-8322
; Sequence 8322, Application US/11434137
; Publication No. US20060210579A1
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 8322
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-137-8322

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  Best Local Similarity   66.7%;  Pred. No. 8e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              |:||:|
Db          7 TSWLSK 12
```

```
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S42364
aromatic-amino-acid transaminase (EC 2.6.1.57) II [validated] - Thermococcus litoralis
C;Species: Thermococcus litoralis
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: S42364
R;Andreotti, G.; Cubellis, M.V.; Nitti, G.; Sannia, G.; Mai, X.; Marino, G.; Adams, M.
Eur. J. Biochem. 220, 543-549, 1994
A;Title: Characterization of aromatic aminotransferases from the hyperthermophilic arc
A;Reference number: S42354; MUID:94170805; PMID:8125113
A;Accession: S42364
A;Molecule type: protein
A;Residues: 1-30
A;Cross-references: UNIPROT:Q9UWK8; UNIPARC:UPI00000629CB
C;Superfamily: aspartate transaminase
C;Keywords: aminotransferase

  Query Match             24.5%;  Score 24;  DB 2;  Length 30;
  Best Local Similarity   50.0%;  Pred. No. 2.6e+03;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWLAKV 7
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Db         12 SWIAKL 17
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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

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Perfect score: 102
Sequence: 1 TKAIINYQYNQYTEEEKNN 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
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3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 102 | 100.0 | 19 | 9 | ADW11062 | Adw11062 Clostridi |
| 2 | 102 | 100.0 | 27 | 9 | ADW11114 | Adw11114 Clostridi |
| 3 | 80 | 78.4 | 15 | 9 | ADZ69805 | Adz69805 Botulinum |

RESULT 30
AEF23970
ID  AEF23970 standard; peptide; 10 AA.
XX
AC  AEF23970;
XX
DT  09-MAR-2006  (first entry)
XX
DE  Factor 8 inhibitor blocking peptide S2/74.
XX
KW  Factor 8 inhibitor; vaccine; hemophilia A; Hemostatic.
XX
OS  Synthetic.
XX
PN  WO2006003183-A1.
XX
PD  12-JAN-2006.
XX
PF  01-JUL-2005; 2005WO-EP053139.
XX
PR  02-JUL-2004; 2004EP-00015586.
XX
PA  (JUNG/) JUNGBAUER A.
XX
PI  Jungbauer A;
XX
DR  WPI; 2006-109510/11.
XX
PT  New peptides that block the effects of factor 8 inhibitors, useful in the
PT  treatment of hemophilia A.
XX
PS  Claim 7; Page 24; 51pp; German.
XX
CC  This invention describes novel peptides that block the effects of Factor
CC  8 inhibitors. The peptides contain at least two Tyr; at least one aa
CC  that, under physiological conditions, carries a positive or negative
CC  overall charge; at least one aa with a hydrophobic aromatic residue; at
CC  the N-terminus one of Pro, Arg, Tyr or Phe; at the C-terminus one of Asp,
CC  Arg, Lys, His or Phe; but no Cys and/or Val-Val. The peptides may be
CC  conjugated to a compound that extends its half-life in vivo, e.g.
CC  poly(ethylene glycol), dextran or agarose, and may include aa with the D-
CC  configuration. The peptides block the autoantibodies/alloantibodies
CC  directed against Factor 8, where these Ab inactivate Factor 8 so that
CC  exogenously administered Factor 8 is no longer effective. When used as
CC  vaccines they generate anti-idiotype antibodies that ensure long-term
CC  protection. Since the peptides are relatively small, they block only the
CC  binding site of Factor 8 inhibitors; they can interfere with inhibitory
CC  antibodies having different epitope recognition patterns; generate an
CC  immune response only against the epitope of interest; are easily prepared
CC  ; are unlikely to induce an immune response or have significant side
CC  effects, and only affected subjects need to be treated. The novel
CC  peptides are useful for the treatment of hemophilia A.
XX
SQ  Sequence 10 AA;

Query Match  33.3%;  Score 34;  DB 10;  Length 10;
Best Local Similarity  71.4%;  Pred. No. 2e+02;
Matches  5;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  6 NYQYNQY 12
      :|||||:

```
Db          2 HYQYNQF 8
```

```
RESULT 50
AEF23919
ID   AEF23919 standard; peptide; 10 AA.
XX
AC   AEF23919;
XX
DT   09-MAR-2006  (first entry)
XX
DE   Factor 8 inhibitor blocking peptide S2/23.
XX
KW   Factor 8 inhibitor; vaccine; hemophilia A; Hemostatic.
XX
OS   Synthetic.
XX
PN   WO2006003183-A1.
XX
PD   12-JAN-2006.
XX
PF   01-JUL-2005; 2005WO-EP053139.
XX
PR   02-JUL-2004; 2004EP-00015586.
XX
PA   (JUNG/) JUNGBAUER A.
XX
PI   Jungbauer A;
XX
DR   WPI; 2006-109510/11.
XX
PT   New peptides that block the effects of factor 8 inhibitors, useful in the
PT   treatment of hemophilia A.
XX
PS   Claim 7; Page 24; 51pp; German.
XX
CC   This invention describes novel peptides that block the effects of Factor
CC   8 inhibitors. The peptides contain at least two Tyr; at least one aa
CC   that, under physiological conditions, carries a positive or negative
CC   overall charge; at least one aa with a hydrophobic aromatic residue; at
CC   the N-terminus one of Pro, Arg, Tyr or Phe; at the C-terminus one of Asp,
CC   Arg, Lys, His or Phe; but no Cys and/or Val-Val. The peptides may be
CC   conjugated to a compound that extends its half-life in vivo, e.g.
CC   poly(ethylene glycol), dextran or agarose, and may include aa with the D-
CC   configuration. The peptides block the autoantibodies/alloantibodies
CC   directed against Factor 8, where these Ab inactivate Factor 8 so that
CC   exogenously administered Factor 8 is no longer effective. When used as
CC   vaccines they generate anti-idiotype antibodies that ensure long-term
CC   protection. Since the peptides are relatively small, they block only the
CC   binding site of Factor 8 inhibitors; they can interfere with inhibitory
CC   antibodies having different epitope recognition patterns; generate an
CC   immune response only against the epitope of interest; are easily prepared
CC   ; are unlikely to induce an immune response or have significant side
CC   effects, and only affected subjects need to be treated. The novel
CC   peptides are useful for the treatment of hemophilia A.
XX
SQ   Sequence 10 AA;

  Query Match             32.4%;  Score 33;  DB 10;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YQYNQY 12
              |||||:
```

Db 3 YQYNQF 8

Search completed: November 1, 2006, 13:11:52
Job time : 112.564 secs

SCORE 1.3 BuildDate: 12/06/2005

```
RESULT 43
US-09-879-792-25
; Sequence 25, Application US/09879792
; Patent No. 6734006
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Yonghong
;  APPLICANT:  Gedrich, Richard
;  TITLE OF INVENTION: Regulation of Human Transmembrane Serine
;  TITLE OF INVENTION:  Protease
;  FILE REFERENCE: 02973.00035
;  CURRENT APPLICATION NUMBER: US/09/879,792
;  CURRENT FILING DATE:  2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/211,224
;  PRIOR FILING DATE: 2000-06-13
;  PRIOR APPLICATION NUMBER: US 60/283,353
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: US 60/283,648
;  PRIOR FILING DATE: 2001-04-16
;  PRIOR APPLICATION NUMBER: PCT _________ (Docket No. 6734006 LIO-81-WO)
;  PRIOR FILING DATE: 2001-06-12
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: BLOCKS BL00495L
US-09-879-792-25

  Query Match             30.4%;  Score 31;  DB 2;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IINYQYN 10
              ||||:|:
Db          6 IINYEYD 12
```

```
RESULT 44
US-08-485-588-11
; Sequence 11, Application US/08485588
; Patent No. 5688938
;  GENERAL INFORMATION:
;    APPLICANT:  Edward M. Brown
;    APPLICANT:  Steven C. Hebert
;    APPLICANT:  Forrest H. Fuller
;    APPLICANT:  James E. Garrett, Jr.
;    TITLE OF INVENTION:  CALCIUM RECEPTOR-ACTIVE
;    TITLE OF INVENTION:  MOLECULES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  First Interstate World Center
;      STREET:  Suite 4700
;      STREET:  633 West Fifth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  FASTSEQ
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,588
;      FILING DATE:  7 June, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:  9
;      APPLICATION NUMBER:  08/353,784
;      FILING DATE:  9 December, 1994
;      APPLICATION NUMBER:  PCT/US/94/12117
;      FILING DATE:  21 October, 1994
;      APPLICATION NUMBER:  U.S. 08/292,827
;      FILING DATE:  23 August, 1994
;      APPLICATION NUMBER:  U.S. 08/141,248
;      FILING DATE:  22 October, 1993
;      APPLICATION NUMBER:  U.S. 08/009,389
;      FILING DATE:  23 February, 1993
;      APPLICATION NUMBER:  U.S. 08/017,127
;      FILING DATE:  12 February, 1993
;      APPLICATION NUMBER:  U.S. 07/934,161
;      FILING DATE:  21 August, 1992
;      APPLICATION NUMBER:  U.S. 07/834,044
;      FILING DATE:  11 February, 1992
;      APPLICATION NUMBER:  U.S. 07/749,451
;      FILING DATE:  23 August, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heber, Sheldon O.
;      REGISTRATION NUMBER:  38,179
;      REFERENCE/DOCKET NUMBER:  213/005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  19 amino acids
;      TYPE:  amino acids
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-485-588-11

  Query Match             30.4%;  Score 31;  DB 1;  Length 19;
  Best Local Similarity   62.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 NQYTEEEK 17
              :||::|||
Db          9 SQYSDEEK 16
```

```
RESULT 1
US-10-715-810-80
; Sequence 80, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 745-759)
US-10-715-810-80

  Query Match             78.4%;  Score 80;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AIINYQYNQYTEEEK 17
              |||||||||||||||
Db          1 AIINYQYNQYTEEEK 15
```

```
RESULT 31
US-10-526-062-15
; Sequence 15, Application US/10526062
; Publication No. US20060141563A1
; GENERAL INFORMATION:
;  APPLICANT: Biemans, Ralph
;  APPLICANT:  Denoel, Philippe
;  APPLICANT:  Feron, Christiane
;  APPLICANT:  Goraj, Karine
;  APPLICANT:  Kortekaas, Jeroen
;  APPLICANT:  Poolman, Jan
;  APPLICANT:  Tommassen, Jan
;  APPLICANT:  Weynants, Vincent
;  TITLE OF INVENTION: Mutant Protein and Refolding Method
;  FILE REFERENCE: VB60394
;  CURRENT APPLICATION NUMBER: US/10/526,062
;  CURRENT FILING DATE:  2005-02-28
;  PRIOR APPLICATION NUMBER: PCT/EP03/009634
;  PRIOR FILING DATE: 2003-08-28
;  PRIOR APPLICATION NUMBER: GB 0220199.4
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Neisseria meningitidis
US-10-526-062-15

  Query Match             27.5%;  Score 28;  DB 6;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TEEEKN 18
              |:||||
Db          1 TDEEKN 6
```

```
RESULT 25
JC2059
homeobox 4 protein - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JC2059
R;Feng, X.H.; Kung, S.D.
Biochem. Biophys. Res. Commun. 198, 1012-1019, 1994
A;Title: Identification of differentially expressed members of tobacco homeobox famili
A;Reference number: JC2057; MUID:94161708; PMID:7509595
A;Accession: JC2059
A;Molecule type: DNA
A;Residues: 1-19
A;Cross-references: UNIPROT:Q9SXV1; UNIPARC:UPI000017B0A8
A;Experimental source: leaf
C;Genetics:
A;Gene: Hot4
C;Keywords: homeobox

  Query Match             25.5%;  Score 26;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 EEEKN 18
              |||||
Db          1 EEEKN 5
```

```
RESULT 1
US-10-142-238A-70
; Sequence 70, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
;  APPLICANT: Bielicki, John K.
;  TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
;  FILE REFERENCE: IB-1705
;  CURRENT APPLICATION NUMBER: US/10/142,238A
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/289,944
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(22)
;   OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-70

  Query Match             43.0%;  Score 40;  DB 4;  Length 22;
  Best Local Similarity   43.8%;  Pred. No. 31;
  Matches    7;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 LNESINKAMININKFL 18
              | :|: : : |:||||
Db          3 LKDSLEQCLNNMNKFL 18
```

```
 Sequence 387, Application US/11199853
; Publication No. US20060216309A1
;  GENERAL INFORMATION:
;    APPLICANT:  David William Holden
;    TITLE OF INVENTION:  Identification of Genes
;    NUMBER OF SEQUENCES:  501
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/199,853
;      FILING DATE:  09-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/871,355
;      FILING DATE:  09-JUN-1997
;      APPLICATION NUMBER:  PCT/GB95/02875
;      FILING DATE:  11-DEC-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  RPMS 101 CON
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 873-8794
;      TELEFAX:  (404) 873-8795
;  INFORMATION FOR SEQ ID NO:  387:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-11-199-853-387

  Query Match             32.3%;  Score 30;  DB 7;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ININKF 17
              ||:|||
Db         10 INVNKF 15
```

```
RESULT 37
S12171
H+-transporting two-sector ATPase (EC 3.6.3.14) lipid-binding protein - fission yeast
C;Species: mitochondrion Schizosaccharomyces pombe
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S12171
R;Massardo, D.R.
Nucleic Acids Res. 18, 6429, 1990
A;Title: Nucleotide sequence of the genes encoding tRNA(his), tRNA(pro) and tRNA(gln)
A;Reference number: S12171; MUID:91057135; PMID:2243789
A;Accession: S12171
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-14
A;Cross-references: UNIPROT:P21535; UNIPARC:UPI000016D64B; EMBL:X54552; NID:g13659; PI
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC2
C;Keywords: hydrolase; mitochondrion

  Query Match             23.7%;  Score 22;  DB 2;  Length 14;
  Best Local Similarity   50.0%;  Pred. No. 3.5e+03;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LNESIN 8
              :|:|:|
Db          7 INDSLN 12
```

```
RESULT 32
P91713_DUGTI
ID   P91713_DUGTI   PRELIMINARY;   PRT;    27 AA.
AC   P91713;
DT   01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1997, sequence version 1.
DT   07-FEB-2006, entry version 23.
DE   Homeodomain protein (Fragment).
GN   Name=DthoxB;
OS   Dugesia tigrina (Planarian).
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC   Paludicola; Dugesiidae; Girardia.
OX   NCBI_TaxID=6162;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97158715; PubMed=9006075;
RA   Bayascas J.R., Castillo E., Munoz-Marmol A.M., Salo E.B.;
RT   "Planarian Hox genes: novel patterns of expression during
RT   regeneration.";
RL   Development 124:141-148(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99016215; PubMed=9799427; DOI=10.1007/s004270050204;
RA   Bayascas J.R., Castillo E., Salo E.B.;
RT   "Platyhelminthes have a hox code differentially activated during
RT   regeneration, with genes closely related to those of spiralian
RT   protostomes.";
RL   Dev. Genes Evol. 208:467-473(1998).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X95415; CAA64695.1; -; Genomic_DNA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001356; Homeobox.
DR   Pfam; PF00046; Homeobox; 1.
DR   PRINTS; PR00024; HOMEOBOX.
KW   DNA-binding; Homeobox; Nuclear protein.
FT   NON_TER       1      1
FT   NON_TER      27     27
SQ   SEQUENCE   27 AA;  3339 MW;  9B4F2D5E657EB7F8 CRC64;

  Query Match             30.1%;  Score 28;  DB 2;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 7.7e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 NINKFL 18
              ||||:|
Db          1 NINKYL 6
```

```
RESULT 34
Q4YZJ6_PLABE
ID   Q4YZJ6_PLABE   PRELIMINARY;   PRT;    30 AA.
AC   Q4YZJ6;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Hypothetical protein (Fragment).
GN   ORFNames=PB103726.00.0;
OS   Plasmodium berghei.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5821;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15637271; DOI=10.1126/science.1103717;
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA   Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA   Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAI01001503; CAH96546.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   30 AA;  3732 MW;  EFDC5780BC5A42A9 CRC64;

  Query Match             30.1%;  Score 28;  DB 2;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 8.5e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 NINKFL 18
              ||||:|
Db          8 NINKYL 13
```

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_771_789
Perfect score: 93
Sequence: 1 SKLNESINKAMININKFLN 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 93 | 100.0 | 19 | 9 | ADW11064 | Adw11064 Clostridi |
| 2 | 93 | 100.0 | 27 | 9 | ADW11115 | Adw11115 Clostridi |
| 3 | 46 | 49.5 | 27 | 9 | ADW11116 | Adw11116 Clostridi |
| 4 | 40 | 43.0 | 22 | 7 | ADC29695 | Adc29695 Antioxida |
| 5 | 40 | 43.0 | 23 | 3 | AAY89467 | Aay89467 Core poly |
| 6 | 40 | 43.0 | 23 | 3 | AAY89409 | Aay89409 Core poly |

RESULT 25
ADZ15100
ID  ADZ15100 standard; peptide; 22 AA.
XX
AC  ADZ15100;
XX
DT  16-JUN-2005  (first entry)
XX
DE  Picornavirus 2A-like NPG/P peptide #45.
XX
KW  cancer; Cytostatic; neoplasm.
XX
OS  Picornaviridae.
XX
PN  WO2005030139-A2.
XX
PD  07-APR-2005.
XX
PF  23-SEP-2004; 2004WO-US031504.
XX
PR  26-SEP-2003; 2003US-0506182P.
XX
PA  (NOVS ) NOVARTIS AG.
XX
PI  Hallenbeck PL,  Hay CM,  Ganesh S,  Police SR,  Xu L,  Yang J;
PI  Cheng C;
XX
DR  WPI; 2005-262902/27.
XX
PT  New Seneca Valley virus nucleic acid or polypeptide, useful in preparing
PT  a composition for treating cancer or inhibiting cancer progression.
XX
PS  Disclosure; Fig 70; 198pp; English.
XX
CC  The invention relates to a new isolated Seneca Valley virus (SVV) nucleic
CC  acid. The nucleic acid is useful in preparing a composition for treating
CC  cancer or inhibiting cancer progression. The present sequence represents
CC  the amino acid sequence of a picornavirus 2A-like NPG/P peptide.
XX
SQ  Sequence 22 AA;

  Query Match             34.3%;  Score 35;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 KFLNQC 7
              ||||||
Db          8 KFLNQC 13

785-803

```
RESULT 1
US-11-335-891-92
; Sequence 92, Application US/11335891
; Publication No. US20060159659A1
; GENERAL INFORMATION:
;  APPLICANT: HALLENBECK, PAUL
;  TITLE OF INVENTION: SENECA VALLEY VIRUS BASED COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  TREATING DISEASE
;  FILE REFERENCE: 287037.127US2
;  CURRENT APPLICATION NUMBER: US/11/335,891
;  CURRENT FILING DATE:  2006-01-19
;  PRIOR APPLICATION NUMBER: 60/506,182
;  PRIOR FILING DATE: 2003-09-26
;  PRIOR APPLICATION NUMBER: PCT/US2004/031504
;  PRIOR FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: 60/664,442
;  PRIOR FILING DATE: 2005-03-23
;  PRIOR APPLICATION NUMBER: 60/726,313
;  PRIOR FILING DATE: 2005-10-13
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 92
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Ljungan virus
US-11-335-891-92

  Query Match            34.3%;  Score 35;  DB 7;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 KFLNQC 7
              ||||||
Db          8 KFLNQC 13
```

```
RESULT 28
ADZ15102
ID   ADZ15102 standard; peptide; 22 AA.
XX
AC   ADZ15102;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Picornavirus 2A-like NPG/P peptide #47.
XX
KW   cancer; Cytostatic; neoplasm.
XX
OS   Picornaviridae.
XX
PN   WO2005030139-A2.
XX
PD   07-APR-2005.
XX
PF   23-SEP-2004; 2004WO-US031504.
XX
PR   26-SEP-2003; 2003US-0506182P.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Hallenbeck PL,  Hay CM,  Ganesh S,  Police SR,  Xu L,  Yang J;
PI   Cheng C;
XX
DR   WPI; 2005-262902/27.
XX
PT   New Seneca Valley virus nucleic acid or polypeptide, useful in preparing
PT   a composition for treating cancer or inhibiting cancer progression.
XX
PS   Disclosure; Fig 70; 198pp; English.
XX
CC   The invention relates to a new isolated Seneca Valley virus (SVV) nucleic
CC   acid. The nucleic acid is useful in preparing a composition for treating
CC   cancer or inhibiting cancer progression. The present sequence represents
CC   the amino acid sequence of a picornavirus 2A-like NPG/P peptide.
XX
SQ   Sequence 22 AA;

  Query Match             34.3%;  Score 35;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 KFLNQC 7
              ||||||
Db          8 KFLNQC 13
```

RESULT 45
ADW30996
ID  ADW30996 standard; peptide; 9 AA.
XX
AC  ADW30996;
XX
DT  10-MAR-2005  (first entry)
XX
DE  HLA binding epitope #1746.
XX
KW  Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW  MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW  viral disease; cancer.
XX
OS  Unidentified.
XX
PN  WO2003040165-A2.
XX
PD  15-MAY-2003.
XX
PF  18-OCT-2001; 2001WO-US051650.
XX
PR  19-OCT-2000; 2000US-0242350P.
PR  20-APR-2001; 2001US-0285624P.
XX
PA  (EPIM-) EPIMMUNE INC.
XX
PI  Sette A,  Sidney J,  Southwood S;
XX
DR  WPI; 2003-441519/41.
XX
PT  New composition comprising at least one peptide having allele-specific
PT  binding motifs for HLA, useful for preventing, treating or diagnosing
PT  viral diseases and cancer.
XX
PS  Claim 1; Page 52-379; 382pp; English.
XX
CC  The invention relates to a composition comprising at least one peptide
CC  having an isolated, prepared epitope selected from any of the sequences
CC  from 30 lists given in the specification. Also disclosed is a method for
CC  inducing a cytotoxic T cell response against a pre-selected antigen in a
CC  patient expressing a specific MHC class I allele by contacting cytotoxic
CC  T cells from the patient with the composition cited above. The
CC  composition comprises an epitope that is joined by an amino acid linker.
CC  The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC  bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC  -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC  binds to a complex of the HLA molecule and the epitope. Specifically
CC  claimed are peptides having allele-specific binding motifs for HLA. The
CC  compositions and methods are useful for preventing, treating or
CC  diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC  diagnostic agents for evaluating immune responses, for making antibodies
CC  and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
CC  ADW37745 represent epitopes of the invention as given in Tables 2-31.
XX
SQ  Sequence 9 AA;

  Query Match             30.4%;  Score 31;  DB 7;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 2.1e+06;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

```
Qy          13 MNSMIPY 19
               :|||::||
Db           2 LNSLVPY 8
```

```
RESULT 1
US-10-715-810-13
; Sequence 13, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 787-806)
US-10-715-810-13

  Query Match             89.2%;  Score 91;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

```
RESULT 2
US-10-715-810-28
; Sequence 28, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 350-369)
US-10-715-810-28

  Query Match             89.2%;  Score 91;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

```
RESULT 3
US-10-715-810-83
; Sequence 83, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 787-806)
US-10-715-810-83

  Query Match             89.2%;  Score 91;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

```
RESULT 40
US-10-378-173-114
; Sequence 114, Application US/10378173
; Publication No. US20030232014A1
; GENERAL INFORMATION:
;  APPLICANT: Burke et al.
;  TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
;  FILE REFERENCE: MDSP-P01-023
;  CURRENT APPLICATION NUMBER: US/10/378,173
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: 60/360787
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorylated peptide
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: phosphorylation
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (8)..(8)
;   OTHER INFORMATION: phosphorylation
US-10-378-173-114

  Query Match             29.4%;  Score 30;  DB 4;  Length 11;
  Best Local Similarity   55.6%;  Pred. No. 5.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 SYLMNSMIP 18
              :|:|||  |
Db          2 AYMMNSQSP 10
```

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_785_803
Perfect score: 102
Sequence: 1 NKFLNQCSVSYLMNSMIPY 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 102 | 100.0 | 19 | 9 | ADW11065 | Adw11065 Clostridi |
| 2 | 102 | 100.0 | 27 | 9 | ADW11116 | Adw11116 Clostridi |
| 3 | 91 | 89.2 | 20 | 9 | ADZ69738 | Adz69738 Botulinum |
| 4 | 91 | 89.2 | 20 | 9 | ADZ69808 | Adz69808 Botulinum |
| 5 | 91 | 89.2 | 20 | 9 | ADZ69753 | Adz69753 Botulinum |
| 6 | 49 | 48.0 | 27 | 9 | ADW11115 | Adw11115 Clostridi |
| 7 | 41 | 40.2 | 16 | 6 | ABP83366 | Abp83366 G protein |
| 8 | 38 | 37.3 | 26 | 8 | ABO53994 | Abo53994 Human |

# SCORE Search Results Details for Application 10821669 and Search Result us-10-821-669-1_copy_813_831.szlm30.rup.

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start

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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 13:04:05 ; Search time 111.239 Seconds
(without alignments)
157.995 Million cell updates/sec

Title: US-10-821-669-1_COPY_813_831
Perfect score: 94
Sequence: 1 ASLKDALLKYIYDNRGTLI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 42 | 44.7 | 22 | 2 | Q4YAS5_PLABE | Q4yas5 plasmodium |
| 2 | 41 | 43.6 | 26 | 2 | Q4Y322_PLACH | Q4y322 plasmodium |
| 3 | 35 | 37.2 | 28 | 2 | P89161_SIVCZ | P89161 chimpanzee |
| 4 | 34 | 36.2 | 20 | 2 | Q9R4D2_HAEPA | Q9r4d2 haemophilus |

| | | | | | | |
|---|---|---|---|---|---|---|
| 5 | 32 | 34.0 | 28 | 2 | Q4X2V6_PLACH | Q4x2v6 plasmodium |
| 6 | 31 | 33.0 | 21 | 2 | O25621_HELPY | O25621 helicobacte |
| 7 | 31 | 33.0 | 23 | 2 | Q4Z2T5_PLABE | Q4z2t5 plasmodium |
| 8 | 31 | 33.0 | 25 | 2 | Q4YGW4_PLABE | Q4ygw4 plasmodium |
| 9 | 31 | 33.0 | 27 | 2 | Q4X7E7_PLACH | Q4x7e7 plasmodium |
| 10 | 31 | 33.0 | 27 | 2 | Q4XIW2_PLACH | Q4xiw2 plasmodium |
| 11 | 31 | 33.0 | 29 | 2 | Q57I38_SALCH | Q57i38 salmonella |
| 12 | 31 | 33.0 | 29 | 2 | Q8ZL14_SALTY | Q8zl14 salmonella |
| 13 | 31 | 33.0 | 30 | 2 | Q4YJP6_PLABE | Q4yjp6 plasmodium |
| 14 | 30 | 31.9 | 21 | 1 | OMP1_HAEPR | P80369 haemophilus |
| 15 | 30 | 31.9 | 26 | 2 | Q4RDE7_TETNG | Q4rde7 tetraodon n |
| 16 | 30 | 31.9 | 29 | 2 | O62784_ISOMA | O62784 isoodon mac |
| 17 | 29 | 30.9 | 17 | 2 | Q9QV51_9MURI | Q9qv51 mus sp. 60 |
| 18 | 29 | 30.9 | 20 | 1 | OMPH_HAEGA | P80451 haemophilus |
| 19 | 28 | 29.8 | 10 | 2 | Q9PRU1_CYNPY | Q9pru1 cynops pyrr |
| 20 | 28 | 29.8 | 13 | 2 | Q6TKR2_HUMAN | Q6tkr2 homo sapien |
| 21 | 28 | 29.8 | 22 | 2 | Q96Q57_HUMAN | Q96q57 homo sapien |
| 22 | 28 | 29.8 | 23 | 2 | Q7RLB8_PLAYO | Q7rlb8 plasmodium |
| 23 | 28 | 29.8 | 24 | 2 | Q4XDJ9_PLACH | Q4xdj9 plasmodium |
| 24 | 28 | 29.8 | 24 | 2 | Q9R5S1_ENTHR | Q9r5s1 enterococcu |
| 25 | 28 | 29.8 | 25 | 2 | Q56CB0_9HIV1 | Q56cb0 human immun |
| 26 | 28 | 29.8 | 26 | 2 | Q6EML2_MELGA | Q6eml2 meleagris g |
| 27 | 28 | 29.8 | 26 | 2 | Q6EML3_CHICK | Q6eml3 gallus gall |
| 28 | 28 | 29.8 | 27 | 2 | Q6U210_HUMAN | Q6u210 homo sapien |
| 29 | 28 | 29.8 | 27 | 2 | Q4X644_PLACH | Q4x644 plasmodium |
| 30 | 28 | 29.8 | 30 | 2 | Q4YER7_PLABE | Q4yer7 plasmodium |
| 31 | 27.5 | 29.3 | 30 | 2 | Q4Y299_PLACH | Q4y299 plasmodium |
| 32 | 27 | 28.7 | 19 | 2 | Q53502_LACPA | Q53502 lactobacill |
| 33 | 27 | 28.7 | 20 | 1 | PEPT_FUSNP | P81207 fusobacteri |
| 34 | 27 | 28.7 | 20 | 2 | Q4XVG2_PLACH | Q4xvg2 plasmodium |
| 35 | 27 | 28.7 | 20 | 2 | Q4YMR5_PLABE | Q4ymr5 plasmodium |
| 36 | 27 | 28.7 | 20 | 2 | Q9PS63_CHICK | Q9ps63 gallus gall |
| 37 | 27 | 28.7 | 22 | 1 | OMPH_PASGA | P80454 pasteurella |
| 38 | 27 | 28.7 | 22 | 1 | OMPH_PASVO | P80452 pasteurella |
| 39 | 27 | 28.7 | 23 | 2 | Q8MFJ9_9FILI | Q8mfj9 hymenophyll |
| 40 | 27 | 28.7 | 23 | 2 | Q8MFK5_9FILI | Q8mfk5 hymenophyll |
| 41 | 27 | 28.7 | 24 | 2 | Q4X3E2_PLACH | Q4x3e2 plasmodium |
| 42 | 27 | 28.7 | 24 | 2 | Q4Y887_PLACH | Q4y887 plasmodium |
| 43 | 27 | 28.7 | 26 | 1 | PSAE_SYNVU | P20900 synechococc |
| 44 | 27 | 28.7 | 26 | 2 | Q4XR84_PLACH | Q4xr84 plasmodium |
| 45 | 27 | 28.7 | 28 | 2 | Q4YGQ5_PLABE | Q4ygq5 plasmodium |
| 46 | 27 | 28.7 | 28 | 2 | Q7R7G7_PLAYO | Q7r7g7 plasmodium |
| 47 | 27 | 28.7 | 29 | 2 | Q4X4G9_PLACH | Q4x4g9 plasmodium |
| 48 | 27 | 28.7 | 29 | 2 | Q4Y032_PLACH | Q4y032 plasmodium |
| 49 | 27 | 28.7 | 29 | 2 | Q4YBJ7_PLABE | Q4ybj7 plasmodium |
| 50 | 27 | 28.7 | 30 | 2 | Q4XEF3_PLACH | Q4xef3 plasmodium |
| 51 | 27 | 28.7 | 30 | 2 | Q7RGP6_PLAYO | Q7rgp6 plasmodium |
| 52 | 27 | 28.7 | 30 | 2 | Q65TQ7_MANSM | Q65tq7 mannheimia |
| 53 | 26.5 | 28.2 | 20 | 2 | Q63667_RAT | Q63667 rattus norv |
| 54 | 26.5 | 28.2 | 23 | 2 | Q5H797_9NEOP | Q5h797 hodotermops |
| 55 | 26 | 27.7 | 15 | 2 | Q70Y59_ROSOF | Q70y59 rosmarinus |
| 56 | 26 | 27.7 | 15 | 2 | Q9R4K9_SPIME | Q9r4k9 spiroplasma |
| 57 | 26 | 27.7 | 19 | 2 | Q9BVX6_HUMAN | Q9bvx6 homo sapien |
| 58 | 26 | 27.7 | 19 | 2 | Q4XUW5_PLACH | Q4xuw5 plasmodium |
| 59 | 26 | 27.7 | 19 | 2 | Q4XZW1_PLACH | Q4xzw1 plasmodium |
| 60 | 26 | 27.7 | 19 | 2 | Q70Y73_9LAMI | Q70y73 pycnostachy |
| 61 | 26 | 27.7 | 20 | 2 | Q9TRM7_BOVIN | Q9trm7 bos taurus |
| 62 | 26 | 27.7 | 20 | 2 | Q9R5E3_AERHY | Q9r5e3 aeromonas h |
| 63 | 26 | 27.7 | 21 | 1 | OMP1_ACTEU | P80443 actinobacil |
| 64 | 26 | 27.7 | 21 | 1 | OMP1_ACTPL | P80368 actinobacil |
| 65 | 26 | 27.7 | 21 | 1 | OMP1_ACTSU | P80442 actinobacil |

| | | | | | | |
|---|---|---|---|---|---|---|
| 66 | 26 | 27.7 | 22 | 2 | Q4YG47_PLABE | Q4yg47 plasmodium |
| 67 | 26 | 27.7 | 22 | 2 | Q9TC82_CENEN | Q9tc82 centropomus |
| 68 | 26 | 27.7 | 22 | 2 | Q9TC84_9PERO | Q9tc84 centropomus |
| 69 | 26 | 27.7 | 23 | 2 | Q4XH19_PLACH | Q4xh19 plasmodium |
| 70 | 26 | 27.7 | 23 | 2 | Q4Y4S8_PLACH | Q4y4s8 plasmodium |
| 71 | 26 | 27.7 | 24 | 2 | Q4XS89_PLACH | Q4xs89 plasmodium |
| 72 | 26 | 27.7 | 25 | 2 | Q4YSL4_PLABE | Q4ysl4 plasmodium |
| 73 | 26 | 27.7 | 26 | 2 | Q684V1_9SCOR | Q684v1 mesobuthus |
| 74 | 26 | 27.7 | 27 | 2 | Q06699_YEAST | Q06699 saccharomyc |
| 75 | 26 | 27.7 | 27 | 2 | Q4YHV3_PLABE | Q4yhv3 plasmodium |
| 76 | 26 | 27.7 | 28 | 2 | Q4XCS0_PLACH | Q4xcs0 plasmodium |
| 77 | 26 | 27.7 | 28 | 2 | Q4XFN5_PLACH | Q4xfn5 plasmodium |
| 78 | 26 | 27.7 | 28 | 2 | Q4XR83_PLACH | Q4xr83 plasmodium |
| 79 | 26 | 27.7 | 28 | 2 | Q4YBP0_PLABE | Q4ybp0 plasmodium |
| 80 | 26 | 27.7 | 28 | 2 | Q4YEZ4_PLABE | Q4yez4 plasmodium |
| 81 | 26 | 27.7 | 28 | 2 | Q5G7D5_9HIV1 | Q5g7d5 human immun |
| 82 | 26 | 27.7 | 29 | 1 | ATPA_BRYMA | P26965 bryopsis ma |
| 83 | 26 | 27.7 | 29 | 2 | Q46303_CLOPE | Q46303 clostridium |
| 84 | 26 | 27.7 | 29 | 2 | Q8CJ37_MOUSE | Q8cj37 mus musculu |
| 85 | 26 | 27.7 | 30 | 2 | Q7RT29_PLAYO | Q7rt29 plasmodium |
| 86 | 26 | 27.7 | 30 | 2 | Q7M313_PIG | Q7m313 sus scrofa |
| 87 | 26 | 27.7 | 30 | 2 | Q3D251_STRAG | Q3d251 streptococc |
| 88 | 26 | 27.7 | 30 | 2 | Q3DNJ4_STRAG | Q3dnj4 streptococc |
| 89 | 26 | 27.7 | 30 | 2 | Q4MN89_BACCE | Q4mn89 bacillus ce |
| 90 | 26 | 27.7 | 30 | 2 | Q2NCJ0_9SPHN | Q2ncj0 erythrobact |
| 91 | 26 | 27.7 | 30 | 2 | Q57CL6_BRUAB | Q57cl6 brucella ab |
| 92 | 26 | 27.7 | 30 | 2 | Q2YRG2_BRUA2 | Q2yrg2 brucella ab |
| 93 | 25.5 | 27.1 | 22 | 2 | Q4Y4T1_PLACH | Q4y4t1 plasmodium |
| 94 | 25.5 | 27.1 | 30 | 1 | Y357_BORBU | O51332 borrelia bu |
| 95 | 25 | 26.6 | 16 | 2 | Q90XT4_PHORB | Q90xt4 phoenicopte |
| 96 | 25 | 26.6 | 18 | 2 | Q53BU2_SCYSP | Q53bu2 scytalopus |
| 97 | 25 | 26.6 | 18 | 2 | Q53BU3_9PASS | Q53bu3 pteroptocho |
| 98 | 25 | 26.6 | 18 | 2 | Q53BU4_9PASS | Q53bu4 chamaeza me |
| 99 | 25 | 26.6 | 18 | 2 | Q53BU5_9DEND | Q53bu5 xiphorhynch |
| 100 | 25 | 26.6 | 18 | 2 | Q53BU6_9DEND | Q53bu6 xiphocolapt |
| 101 | 25 | 26.6 | 18 | 2 | Q53BU7_9DEND | Q53bu7 sittasomus |
| 102 | 25 | 26.6 | 18 | 2 | Q53BU8_9FURN | Q53bu8 nasica long |
| 103 | 25 | 26.6 | 18 | 2 | Q53BU9_9DEND | Q53bu9 xiphorhynch |
| 104 | 25 | 26.6 | 18 | 2 | Q53BV0_9FURN | Q53bv0 glyphorynch |
| 105 | 25 | 26.6 | 18 | 2 | Q53BV1_9DEND | Q53bv1 drymornis b |
| 106 | 25 | 26.6 | 18 | 2 | Q53BV2_9DEND | Q53bv2 dendrocincl |
| 107 | 25 | 26.6 | 18 | 2 | Q53BV4_9DEND | Q53bv4 campylorham |
| 108 | 25 | 26.6 | 18 | 2 | Q53BV5_9FURN | Q53bv5 pygarrhicha |
| 109 | 25 | 26.6 | 18 | 2 | Q53BV6_9FURN | Q53bv6 xenops ruti |
| 110 | 25 | 26.6 | 18 | 2 | Q53BV7_9FURN | Q53bv7 xenops minu |
| 111 | 25 | 26.6 | 18 | 2 | Q53BV8_9FURN | Q53bv8 lochmias ne |
| 112 | 25 | 26.6 | 18 | 2 | Q53BV9_9FURN | Q53bv9 sclerurus s |
| 113 | 25 | 26.6 | 18 | 2 | Q53BW0_9FURN | Q53bw0 sclerurus m |
| 114 | 25 | 26.6 | 18 | 2 | Q53BW1_9FURN | Q53bw1 automolus l |
| 115 | 25 | 26.6 | 18 | 2 | Q53BW2_9FURN | Q53bw2 thripadecte |
| 116 | 25 | 26.6 | 18 | 2 | Q53BW3_9FURN | Q53bw3 philydor at |
| 117 | 25 | 26.6 | 18 | 2 | Q53BW4_9FURN | Q53bw4 berlepschia |
| 118 | 25 | 26.6 | 18 | 2 | Q53BW5_9FURN | Q53bw5 margarornis |
| 119 | 25 | 26.6 | 18 | 2 | Q53BW6_9FURN | Q53bw6 coryphister |
| 120 | 25 | 26.6 | 18 | 2 | Q53BW7_9FURN | Q53bw7 anumbius an |
| 121 | 25 | 26.6 | 18 | 2 | Q53BW8_9FURN | Q53bw8 phacellodom |
| 122 | 25 | 26.6 | 18 | 2 | Q53BW9_9FURN | Q53bw9 asthenes ca |
| 123 | 25 | 26.6 | 18 | 2 | Q53BX0_9FURN | Q53bx0 cranioleuca |
| 124 | 25 | 26.6 | 18 | 2 | Q53BX2_9FURN | Q53bx2 leptasthenu |
| 125 | 25 | 26.6 | 18 | 2 | Q53BX3_9FURN | Q53bx3 furnarius c |
| 126 | 25 | 26.6 | 18 | 2 | Q53BX4_9FURN | Q53bx4 cinclodes f |

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|---|---|---|---|---|---|---|
| 127 | 25 | 26.6 | 18 | 2 | Q53BX5_9FURN | Q53bx5 upucerthia |
| 128 | 25 | 26.6 | 18 | 2 | Q53BX7_9FURN | Q53bx7 geositta ru |
| 129 | 25 | 26.6 | 18 | 2 | Q5XMF3_9AVES | Q5xmf3 oxyura macc |
| 130 | 25 | 26.6 | 18 | 2 | Q5XMF4_9AVES | Q5xmf4 oxyura aust |
| 131 | 25 | 26.6 | 18 | 2 | Q5XMF5_OXYJA | Q5xmf5 oxyura jama |
| 132 | 25 | 26.6 | 18 | 2 | Q5XMF6_OXYVI | Q5xmf6 oxyura vitt |
| 133 | 25 | 26.6 | 18 | 2 | Q5XMF7_9AVES | Q5xmf7 nomonyx dom |
| 134 | 25 | 26.6 | 18 | 2 | Q68LC1_9PASS | Q68lc1 phaenostict |
| 135 | 25 | 26.6 | 18 | 2 | Q68LC2_9PASS | Q68lc2 rhegmatorhi |
| 136 | 25 | 26.6 | 18 | 2 | Q68LC3_9PASS | Q68lc3 gymnopithys |
| 137 | 25 | 26.6 | 18 | 2 | Q68LC4_9PASS | Q68lc4 pithys albi |
| 138 | 25 | 26.6 | 18 | 2 | Q68LC5_9PASS | Q68lc5 myrmornis t |
| 139 | 25 | 26.6 | 18 | 2 | Q68LC6_9PASS | Q68lc6 gymnocichla |
| 140 | 25 | 26.6 | 18 | 2 | Q68LC8_9PASS | Q68lc8 myrmeciza f |
| 141 | 25 | 26.6 | 18 | 2 | Q68LC9_9PASS | Q68lc9 myrmeciza l |
| 142 | 25 | 26.6 | 18 | 2 | Q68LD0_9PASS | Q68ld0 myrmeciza h |
| 143 | 25 | 26.6 | 18 | 2 | Q68LD1_9PASS | Q68ld1 myrmeciza g |
| 144 | 25 | 26.6 | 18 | 2 | Q68LD2_9PASS | Q68ld2 schistocich |
| 145 | 25 | 26.6 | 18 | 2 | Q68LD3_9PASS | Q68ld3 sclateria n |
| 146 | 25 | 26.6 | 18 | 2 | Q68LD4_9PASS | Q68ld4 hypocnemoid |
| 147 | 25 | 26.6 | 18 | 2 | Q68LD5_9PASS | Q68ld5 myrmochanes |
| 148 | 25 | 26.6 | 18 | 2 | Q68LD6_9PASS | Q68ld6 hypocnemis |
| 149 | 25 | 26.6 | 18 | 2 | Q68LD7_9PASS | Q68ld7 dichrozona |
| 150 | 25 | 26.6 | 18 | 2 | Q68LD8_9PASS | Q68ld8 myrmoborus |
| 151 | 25 | 26.6 | 18 | 2 | Q68LD9_9PASS | Q68ld9 neoctantes |
| 152 | 25 | 26.6 | 18 | 2 | Q68LE1_9PASS | Q68le1 cercomacra |
| 153 | 25 | 26.6 | 18 | 2 | Q68LE2_9PASS | Q68le2 myrmorchilu |
| 154 | 25 | 26.6 | 18 | 2 | Q68LE3_9PASS | Q68le3 formicivora |
| 155 | 25 | 26.6 | 18 | 2 | Q68LE4_9PASS | Q68le4 drymophila |
| 156 | 25 | 26.6 | 18 | 2 | Q68LE5_9PASS | Q68le5 terenura hu |
| 157 | 25 | 26.6 | 18 | 2 | Q68LE6_9PASS | Q68le6 myrmotherul |
| 158 | 25 | 26.6 | 18 | 2 | Q68LE7_9PASS | Q68le7 myrmotherul |
| 159 | 25 | 26.6 | 18 | 2 | Q68LE8_MYRAX | Q68le8 myrmotherul |
| 160 | 25 | 26.6 | 18 | 2 | Q68LF0_MYRLE | Q68lf0 myrmotherul |
| 161 | 25 | 26.6 | 18 | 2 | Q68LF2_9PASS | Q68lf2 microrhopia |
| 162 | 25 | 26.6 | 18 | 2 | Q68LF3_9PASS | Q68lf3 herpsilochm |
| 163 | 25 | 26.6 | 18 | 2 | Q68LF4_9PASS | Q68lf4 dysithamnus |
| 164 | 25 | 26.6 | 18 | 2 | Q68LF5_9PASS | Q68lf5 thamnomanes |
| 165 | 25 | 26.6 | 18 | 2 | Q68LF6_9PASS | Q68lf6 thamnistes |
| 166 | 25 | 26.6 | 18 | 2 | Q68LF7_9PASS | Q68lf7 pygiptila s |
| 167 | 25 | 26.6 | 18 | 2 | Q68LF8_9PASS | Q68lf8 megastictus |
| 168 | 25 | 26.6 | 18 | 2 | Q68LF9_9PASS | Q68lf9 thamnophilu |
| 169 | 25 | 26.6 | 18 | 2 | Q68LG0_9PASS | Q68lg0 thamnophilu |
| 170 | 25 | 26.6 | 18 | 2 | Q68LG1_9PASS | Q68lg1 thamnophilu |
| 171 | 25 | 26.6 | 18 | 2 | Q68LG2_9PASS | Q68lg2 thamnophilu |
| 172 | 25 | 26.6 | 18 | 2 | Q68LG4_9PASS | Q68lg4 taraba majo |
| 173 | 25 | 26.6 | 18 | 2 | Q68LG5_9PASS | Q68lg5 batara cine |
| 174 | 25 | 26.6 | 18 | 2 | Q68LG6_9PASS | Q68lg6 hypoedaleus |
| 175 | 25 | 26.6 | 18 | 2 | Q68LG7_9PASS | Q68lg7 mackenziaen |
| 176 | 25 | 26.6 | 18 | 2 | Q68LG8_9PASS | Q68lg8 fredericken |
| 177 | 25 | 26.6 | 18 | 2 | Q6UQQ7_9PASE | Q6uqq7 anomalospiz |
| 178 | 25 | 26.6 | 18 | 2 | Q6UQQ8_9PASS | Q6uqq8 vidua orien |
| 179 | 25 | 26.6 | 18 | 2 | Q6UQQ9_9PASS | Q6uqq9 vidua obtus |
| 180 | 25 | 26.6 | 18 | 2 | Q6UQR0_9PASS | Q6uqr0 vidua hypoc |
| 181 | 25 | 26.6 | 18 | 2 | Q6UQR2_9PASS | Q6uqr2 vidua macro |
| 182 | 25 | 26.6 | 18 | 2 | Q6UQR3_9PASS | Q6uqr3 vidua wilso |
| 183 | 25 | 26.6 | 18 | 2 | Q6UQR4_9PASS | Q6uqr4 vidua camer |
| 184 | 25 | 26.6 | 18 | 2 | Q6UQR5_9PASS | Q6uqr5 vidua raric |
| 185 | 25 | 26.6 | 18 | 2 | Q6UQR6_9PASS | Q6uqr6 vidua regia |
| 186 | 25 | 26.6 | 18 | 2 | Q6UQR7_9PASS | Q6uqr7 vidua fisch |
| 187 | 25 | 26.6 | 18 | 2 | Q90XS9_ANAPL | Q90xs9 anas platyr |

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|---|---|---|---|---|---|---|
| 188 | 25 | 26.6 | 18 | 2 | Q90XT1_9CHAR | Q90xt1 charadrius |
| 189 | 25 | 26.6 | 18 | 2 | Q90XT3_9AVES | Q90xt3 aechmophoru |
| 190 | 25 | 26.6 | 18 | 2 | Q90XT6_GAVST | Q90xt6 gavia stell |
| 191 | 25 | 26.6 | 18 | 2 | Q90XT7_PYGAD | Q90xt7 pygoscelis |
| 192 | 25 | 26.6 | 18 | 2 | Q90XT8_CICNG | Q90xt8 ciconia nig |
| 193 | 25 | 26.6 | 18 | 2 | Q90XT9_NYCNY | Q90xt9 nycticorax |
| 194 | 25 | 26.6 | 18 | 2 | Q90XU5_9AVES | Q90xu5 sula neboux |
| 195 | 25 | 26.6 | 18 | 2 | Q90XU6_9AVES | Q90xu6 phaethon ae |
| 196 | 25 | 26.6 | 18 | 2 | Q68LC7_MYRBR | Q68lc7 myrmeciza b |
| 197 | 25 | 26.6 | 19 | 2 | Q6Y078_9PSIT | Q6y078 amazona ama |
| 198 | 25 | 26.6 | 19 | 2 | Q6Y080_9PSIT | Q6y080 amazona och |
| 199 | 25 | 26.6 | 19 | 2 | Q6Y081_9PSIT | Q6y081 amazona och |
| 200 | 25 | 26.6 | 19 | 2 | Q6Y082_9PSIT | Q6y082 amazona och |
| 201 | 25 | 26.6 | 20 | 2 | Q6LDX5_HUMAN | Q6ldx5 homo sapien |
| 202 | 25 | 26.6 | 20 | 2 | Q7LZU6_9INFA | Q7lzu6 influenza a |
| 203 | 25 | 26.6 | 21 | 2 | Q87575_SIVCZ | Q87575 chimpanzee |
| 204 | 25 | 26.6 | 21 | 2 | Q87585_SIVCZ | Q87585 chimpanzee |
| 205 | 25 | 26.6 | 22 | 2 | Q4XC36_PLACH | Q4xc36 plasmodium |
| 206 | 25 | 26.6 | 22 | 2 | Q4Z392_PLABE | Q4z392 plasmodium |
| 207 | 25 | 26.6 | 22 | 2 | Q4Z5M8_PLABE | Q4z5m8 plasmodium |
| 208 | 25 | 26.6 | 22 | 2 | Q9QWB6_9MURI | Q9qwb6 mus sp. sgp |
| 209 | 25 | 26.6 | 23 | 2 | Q4Y4S6_PLACH | Q4y4s6 plasmodium |
| 210 | 25 | 26.6 | 24 | 2 | Q4Z0G6_PLABE | Q4z0g6 plasmodium |
| 211 | 25 | 26.6 | 25 | 2 | Q4XD90_PLACH | Q4xd90 plasmodium |
| 212 | 25 | 26.6 | 25 | 2 | Q4YG46_PLABE | Q4yg46 plasmodium |
| 213 | 25 | 26.6 | 25 | 2 | Q6YJ06_9RHOD | Q6yj06 porphyra ra |
| 214 | 25 | 26.6 | 25 | 2 | O26056_HELPY | O26056 helicobacte |
| 215 | 25 | 26.6 | 25 | 2 | Q3S9W7_9HIV1 | Q3s9w7 human immun |
| 216 | 25 | 26.6 | 26 | 1 | ACHD_ELEEL | P09691 electrophor |
| 217 | 25 | 26.6 | 26 | 2 | Q91U56_9INFA | Q91u56 influenza a |
| 218 | 25 | 26.6 | 27 | 2 | Q4X3J6_PLACH | Q4x3j6 plasmodium |
| 219 | 25 | 26.6 | 27 | 2 | Q4X3K5_PLACH | Q4x3k5 plasmodium |
| 220 | 25 | 26.6 | 27 | 2 | Q4XAJ2_PLACH | Q4xaj2 plasmodium |
| 221 | 25 | 26.6 | 27 | 2 | Q4XHN8_PLACH | Q4xhn8 plasmodium |
| 222 | 25 | 26.6 | 27 | 2 | Q4XI91_PLACH | Q4xi91 plasmodium |
| 223 | 25 | 26.6 | 27 | 2 | Q4XSN8_PLACH | Q4xsn8 plasmodium |
| 224 | 25 | 26.6 | 27 | 2 | Q6V7V8_CHICK | Q6v7v8 gallus gall |
| 225 | 25 | 26.6 | 28 | 2 | Q4X7K6_PLACH | Q4x7k6 plasmodium |
| 226 | 25 | 26.6 | 28 | 2 | Q4YMK5_PLABE | Q4ymk5 plasmodium |
| 227 | 25 | 26.6 | 29 | 1 | PLMS_SCYCA | P83650 scyliorhinu |
| 228 | 25 | 26.6 | 29 | 2 | Q4XJX6_PLACH | Q4xjx6 plasmodium |
| 229 | 25 | 26.6 | 29 | 2 | Q4XSZ6_PLACH | Q4xsz6 plasmodium |
| 230 | 25 | 26.6 | 29 | 2 | Q6JDN0_CANFA | Q6jdn0 canis famil |
| 231 | 25 | 26.6 | 29 | 2 | Q3CYH8_STRAG | Q3cyh8 streptococc |
| 232 | 25 | 26.6 | 29 | 2 | Q4TF38_TETNG | Q4tf38 tetraodon n |
| 233 | 25 | 26.6 | 30 | 2 | Q35904_SCHPO | Q35904 schizosacch |
| 234 | 25 | 26.6 | 30 | 2 | Q7RJB8_PLAYO | Q7rjb8 plasmodium |
| 235 | 25 | 26.6 | 30 | 2 | Q84JV1_CRYJA | Q84jv1 cryptomeria |
| 236 | 25 | 26.6 | 30 | 2 | Q4SAM1_TETNG | Q4sam1 tetraodon n |
| 237 | 24.5 | 26.1 | 21 | 2 | Q9F7Y5_NEIGO | Q9f7y5 neisseria g |
| 238 | 24.5 | 26.1 | 29 | 2 | O03120_9EMBR | O03120 megaceros v |
| 239 | 24.5 | 26.1 | 29 | 2 | Q7A5V9_STAAN | Q7a5v9 staphylococ |
| 240 | 24.5 | 26.1 | 29 | 2 | Q8NWX8_STAAW | Q8nwx8 staphylococ |
| 241 | 24.5 | 26.1 | 29 | 2 | Q99UH5_STAAM | Q99uh5 staphylococ |
| 242 | 24.5 | 26.1 | 30 | 2 | Q6MKG8_BDEBA | Q6mkg8 bdellovibri |
| 243 | 24 | 25.5 | 14 | 2 | Q4JHP1_9CARY | Q4jhp1 suaeda liao |
| 244 | 24 | 25.5 | 14 | 2 | Q70Y61_9LAMI | Q70y61 ocimum sell |
| 245 | 24 | 25.5 | 14 | 2 | Q6R7V0_9SAUR | Q6r7v0 carlia viva |
| 246 | 24 | 25.5 | 15 | 2 | Q9S8P1_RAPSA | Q9s8p1 raphanus sa |
| 247 | 24 | 25.5 | 16 | 2 | Q6Y079_AMAAE | Q6y079 amazona aes |
| 248 | 24 | 25.5 | 17 | 2 | Q7XB06_MAIZE | Q7xb06 zea mays (m |

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|---|---|---|---|---|---|---|
| 249 | 24 | 25.5 | 17 | 2 | Q4VI71_9SAUR | Q4vi71 actinemys m |
| 250 | 24 | 25.5 | 17 | 2 | Q6R7U8_9SAUR | Q6r7u8 lampropholi |
| 251 | 24 | 25.5 | 17 | 2 | Q6R7U9_9SAUR | Q6r7u9 saproscincu |
| 252 | 24 | 25.5 | 17 | 2 | Q6R7V1_9SAUR | Q6r7v1 carlia rost |
| 253 | 24 | 25.5 | 17 | 2 | Q6R7V2_9SAUR | Q6r7v2 carlia rufi |
| 254 | 24 | 25.5 | 17 | 2 | Q6R7V3_9SAUR | Q6r7v3 carlia fusc |
| 255 | 24 | 25.5 | 17 | 2 | Q6R7V5_9SAUR | Q6r7v5 carlia rhom |
| 256 | 24 | 25.5 | 17 | 2 | Q6R7V6_9SAUR | Q6r7v6 carlia rubr |
| 257 | 24 | 25.5 | 18 | 2 | Q7Y4F7_9CAUD | Q7y4f7 lactococcus |
| 258 | 24 | 25.5 | 18 | 2 | Q7Y4G1_9CAUD | Q7y4g1 lactococcus |
| 259 | 24 | 25.5 | 18 | 2 | Q7XB07_MAIZE | Q7xb07 zea mays (m |
| 260 | 24 | 25.5 | 18 | 2 | Q2PDK6_CLODI | Q2pdk6 clostridium |
| 261 | 24 | 25.5 | 18 | 2 | Q9PXB6_ADE05 | Q9pxb6 human adeno |
| 262 | 24 | 25.5 | 18 | 2 | Q53BV3_9FURN | Q53bv3 deconychura |
| 263 | 24 | 25.5 | 18 | 2 | Q53BX6_9FURN | Q53bx6 geositta te |
| 264 | 24 | 25.5 | 19 | 2 | Q8IVH1_HUMAN | Q8ivh1 homo sapien |
| 265 | 24 | 25.5 | 19 | 2 | Q70Y92_9LAMI | Q70y92 platostoma |
| 266 | 24 | 25.5 | 20 | 2 | Q4XCZ2_PLACH | Q4xcz2 plasmodium |
| 267 | 24 | 25.5 | 20 | 2 | Q4A2D6_9PHYC | Q4a2d6 emiliania h |
| 268 | 24 | 25.5 | 21 | 2 | Q4Y8T8_PLACH | Q4y8t8 plasmodium |
| 269 | 24 | 25.5 | 21 | 2 | Q4YDB9_PLABE | Q4ydb9 plasmodium |
| 270 | 24 | 25.5 | 21 | 2 | Q4YTM1_PLABE | Q4ytm1 plasmodium |
| 271 | 24 | 25.5 | 21 | 2 | Q9RQ26_CLODI | Q9rq26 clostridium |
| 272 | 24 | 25.5 | 22 | 2 | Q6BGN9_DEBHA | Q6bgn9 debaryomyce |
| 273 | 24 | 25.5 | 22 | 2 | Q4X8D6_PLACH | Q4x8d6 plasmodium |
| 274 | 24 | 25.5 | 22 | 2 | Q4YMD8_PLABE | Q4ymd8 plasmodium |
| 275 | 24 | 25.5 | 22 | 2 | Q9MX47_ORYLA | Q9mx47 oryzias lat |
| 276 | 24 | 25.5 | 23 | 2 | Q9UCE3_HUMAN | Q9uce3 homo sapien |
| 277 | 24 | 25.5 | 23 | 2 | Q4YG20_PLABE | Q4yg20 plasmodium |
| 278 | 24 | 25.5 | 23 | 2 | Q5XYL3_BORGA | Q5xyl3 borrelia ga |
| 279 | 24 | 25.5 | 23 | 2 | Q6UK03_VIBCH | Q6uk03 vibrio chol |
| 280 | 24 | 25.5 | 24 | 2 | Q4X4X8_PLACH | Q4x4x8 plasmodium |
| 281 | 24 | 25.5 | 24 | 2 | Q4XCF4_PLACH | Q4xcf4 plasmodium |
| 282 | 24 | 25.5 | 24 | 2 | Q4XY90_PLACH | Q4xy90 plasmodium |
| 283 | 24 | 25.5 | 24 | 2 | Q7RDJ7_PLAYO | Q7rdj7 plasmodium |
| 284 | 24 | 25.5 | 24 | 2 | Q46081_CLOHU | Q46081 clostridium |
| 285 | 24 | 25.5 | 25 | 1 | TFDC1_COMAC | P83115 comamonas a |
| 286 | 24 | 25.5 | 25 | 2 | Q4XMQ2_PLACH | Q4xmq2 plasmodium |
| 287 | 24 | 25.5 | 25 | 2 | Q4Y1J7_PLACH | Q4y1j7 plasmodium |
| 288 | 24 | 25.5 | 25 | 2 | Q4YT11_PLABE | Q4yt11 plasmodium |
| 289 | 24 | 25.5 | 25 | 2 | Q9N150_BOVIN | Q9n150 bos taurus |
| 290 | 24 | 25.5 | 25 | 2 | O49748_ARATH | O49748 arabidopsis |
| 291 | 24 | 25.5 | 25 | 2 | Q56C92_9HIV1 | Q56c92 human immun |
| 292 | 24 | 25.5 | 25 | 2 | Q56CA1_9HIV1 | Q56ca1 human immun |
| 293 | 24 | 25.5 | 25 | 2 | Q56CA7_9HIV1 | Q56ca7 human immun |
| 294 | 24 | 25.5 | 25 | 2 | Q56CA8_9HIV1 | Q56ca8 human immun |
| 295 | 24 | 25.5 | 25 | 2 | Q56CB5_9HIV1 | Q56cb5 human immun |
| 296 | 24 | 25.5 | 25 | 2 | Q56CB7_9HIV1 | Q56cb7 human immun |
| 297 | 24 | 25.5 | 25 | 2 | Q56CB8_9HIV1 | Q56cb8 human immun |
| 298 | 24 | 25.5 | 25 | 2 | Q56CB9_9HIV1 | Q56cb9 human immun |
| 299 | 24 | 25.5 | 25 | 2 | Q56CC0_9HIV1 | Q56cc0 human immun |
| 300 | 24 | 25.5 | 25 | 2 | Q56CC1_9HIV1 | Q56cc1 human immun |
| 301 | 24 | 25.5 | 25 | 2 | Q56CC2_9HIV1 | Q56cc2 human immun |
| 302 | 24 | 25.5 | 25 | 2 | Q56CC3_9HIV1 | Q56cc3 human immun |
| 303 | 24 | 25.5 | 25 | 2 | Q56CC4_9HIV1 | Q56cc4 human immun |
| 304 | 24 | 25.5 | 25 | 2 | Q56CC5_9HIV1 | Q56cc5 human immun |
| 305 | 24 | 25.5 | 25 | 2 | Q56CC6_9HIV1 | Q56cc6 human immun |
| 306 | 24 | 25.5 | 25 | 2 | Q56CC7_9HIV1 | Q56cc7 human immun |
| 307 | 24 | 25.5 | 25 | 2 | Q56CC8_9HIV1 | Q56cc8 human immun |
| 308 | 24 | 25.5 | 25 | 2 | Q56CC9_9HIV1 | Q56cc9 human immun |
| 309 | 24 | 25.5 | 25 | 2 | Q56CD1_9HIV1 | Q56cd1 human immun |

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|---|---|---|---|---|---|---|
| 310 | 24 | 25.5 | 25 | 2 | Q56CD2_9HIV1 | Q56cd2 human immun |
| 311 | 24 | 25.5 | 25 | 2 | Q56CD3_9HIV1 | Q56cd3 human immun |
| 312 | 24 | 25.5 | 25 | 2 | Q56CD4_9HIV1 | Q56cd4 human immun |
| 313 | 24 | 25.5 | 25 | 2 | Q56CD5_9HIV1 | Q56cd5 human immun |
| 314 | 24 | 25.5 | 25 | 2 | Q56CD6_9HIV1 | Q56cd6 human immun |
| 315 | 24 | 25.5 | 25 | 2 | Q56CD7_9HIV1 | Q56cd7 human immun |
| 316 | 24 | 25.5 | 25 | 2 | Q56CD8_9HIV1 | Q56cd8 human immun |
| 317 | 24 | 25.5 | 25 | 2 | Q56CD9_9HIV1 | Q56cd9 human immun |
| 318 | 24 | 25.5 | 25 | 2 | Q56CE0_9HIV1 | Q56ce0 human immun |
| 319 | 24 | 25.5 | 25 | 2 | Q56CE1_9HIV1 | Q56ce1 human immun |
| 320 | 24 | 25.5 | 25 | 2 | Q56CE2_9HIV1 | Q56ce2 human immun |
| 321 | 24 | 25.5 | 25 | 2 | Q56CE3_9HIV1 | Q56ce3 human immun |
| 322 | 24 | 25.5 | 25 | 2 | Q56CE4_9HIV1 | Q56ce4 human immun |
| 323 | 24 | 25.5 | 25 | 2 | Q56CE5_9HIV1 | Q56ce5 human immun |
| 324 | 24 | 25.5 | 25 | 2 | Q56CE6_9HIV1 | Q56ce6 human immun |
| 325 | 24 | 25.5 | 25 | 2 | Q56CE7_9HIV1 | Q56ce7 human immun |
| 326 | 24 | 25.5 | 25 | 2 | Q56CE8_9HIV1 | Q56ce8 human immun |
| 327 | 24 | 25.5 | 25 | 2 | Q56CE9_9HIV1 | Q56ce9 human immun |
| 328 | 24 | 25.5 | 25 | 2 | Q56CF0_9HIV1 | Q56cf0 human immun |
| 329 | 24 | 25.5 | 25 | 2 | Q56CF1_9HIV1 | Q56cf1 human immun |
| 330 | 24 | 25.5 | 25 | 2 | Q56CF2_9HIV1 | Q56cf2 human immun |
| 331 | 24 | 25.5 | 25 | 2 | Q56CF3_9HIV1 | Q56cf3 human immun |
| 332 | 24 | 25.5 | 25 | 2 | Q56CF4_9HIV1 | Q56cf4 human immun |
| 333 | 24 | 25.5 | 25 | 2 | Q58Q98_9HIV1 | Q58q98 human immun |
| 334 | 24 | 25.5 | 25 | 2 | Q58QA5_9HIV1 | Q58qa5 human immun |
| 335 | 24 | 25.5 | 25 | 2 | Q71969_9HIV1 | Q71969 human immun |
| 336 | 24 | 25.5 | 25 | 2 | Q71988_9HIV1 | Q71988 human immun |
| 337 | 24 | 25.5 | 25 | 2 | Q71994_9HIV1 | Q71994 human immun |
| 338 | 24 | 25.5 | 25 | 2 | Q72010_9HIV1 | Q72010 human immun |
| 339 | 24 | 25.5 | 25 | 2 | Q72016_9HIV1 | Q72016 human immun |
| 340 | 24 | 25.5 | 25 | 2 | Q72020_9HIV1 | Q72020 human immun |
| 341 | 24 | 25.5 | 25 | 2 | Q80273_9HIV1 | Q80273 human immun |
| 342 | 24 | 25.5 | 25 | 2 | Q8QDX7_9HIV1 | Q8qdx7 human immun |
| 343 | 24 | 25.5 | 25 | 2 | Q8QDY1_9HIV1 | Q8qdy1 human immun |
| 344 | 24 | 25.5 | 25 | 2 | Q9IQP7_9HIV1 | Q9iqp7 human immun |
| 345 | 24 | 25.5 | 25 | 2 | Q9IQQ7_9HIV1 | Q9iqq7 human immun |
| 346 | 24 | 25.5 | 25 | 2 | Q9IQQ8_9HIV1 | Q9iqq8 human immun |
| 347 | 24 | 25.5 | 25 | 2 | Q9IQQ9_9HIV1 | Q9iqq9 human immun |
| 348 | 24 | 25.5 | 25 | 2 | Q9IQR0_9HIV1 | Q9iqr0 human immun |
| 349 | 24 | 25.5 | 25 | 2 | Q9IQR1_9HIV1 | Q9iqr1 human immun |
| 350 | 24 | 25.5 | 26 | 2 | Q4YJN2_PLABE | Q4yjn2 plasmodium |
| 351 | 24 | 25.5 | 26 | 2 | Q4YQR4_PLABE | Q4yqr4 plasmodium |
| 352 | 24 | 25.5 | 26 | 2 | Q7R9B5_PLAYO | Q7r9b5 plasmodium |
| 353 | 24 | 25.5 | 26 | 2 | Q7X642_MAIZE | Q7x642 zea mays (m |
| 354 | 24 | 25.5 | 26 | 2 | O86138_CLOBU | O86138 clostridium |
| 355 | 24 | 25.5 | 26 | 2 | Q7B304_CLOBU | Q7b304 clostridium |
| 356 | 24 | 25.5 | 26 | 2 | Q4RA30_TETNG | Q4ra30 tetraodon n |
| 357 | 24 | 25.5 | 26 | 2 | Q4PU49_9HIV1 | Q4pu49 human immun |
| 358 | 24 | 25.5 | 26 | 2 | Q4PU54_9HIV1 | Q4pu54 human immun |
| 359 | 24 | 25.5 | 26 | 2 | Q4PU59_9HIV1 | Q4pu59 human immun |
| 360 | 24 | 25.5 | 27 | 1 | HCY5_HOMAM | P82300 homarus ame |
| 361 | 24 | 25.5 | 27 | 1 | KT395_PICKL | P80326 pichia kluy |
| 362 | 24 | 25.5 | 27 | 2 | Q6YJ05_9RHOD | Q6yj05 porphyra ra |
| 363 | 24 | 25.5 | 27 | 2 | Q7X644_MAIZE | Q7x644 zea mays (m |
| 364 | 24 | 25.5 | 27 | 2 | Q6V7G9_VIBCH | Q6v7g9 vibrio chol |
| 365 | 24 | 25.5 | 28 | 2 | Q4X2X3_PLACH | Q4x2x3 plasmodium |
| 366 | 24 | 25.5 | 28 | 2 | Q4X4G5_PLACH | Q4x4g5 plasmodium |
| 367 | 24 | 25.5 | 28 | 2 | Q4YRV9_PLABE | Q4yrv9 plasmodium |
| 368 | 24 | 25.5 | 28 | 2 | Q4G226_COLGU | Q4g226 colobus gue |
| 369 | 24 | 25.5 | 28 | 2 | Q7XB04_MAIZE | Q7xb04 zea mays (m |
| 370 | 24 | 25.5 | 28 | 2 | Q9R4Z2_LACAC | Q9r4z2 lactobacill |

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| 371 | 24 | 25.5 | 29 | 2 | O44023_PARTE | O44023 paramecium |
| 372 | 24 | 25.5 | 29 | 2 | Q5BYX3_SCHJA | Q5byx3 schistosoma |
| 373 | 24 | 25.5 | 29 | 2 | Q56XC2_ARATH | Q56xc2 arabidopsis |
| 374 | 24 | 25.5 | 29 | 2 | Q7X643_MAIZE | Q7x643 zea mays (m |
| 375 | 24 | 25.5 | 30 | 2 | Q25627_ONCVO | Q25627 onchocerca |
| 376 | 24 | 25.5 | 30 | 2 | Q4XG67_PLACH | Q4xg67 plasmodium |
| 377 | 24 | 25.5 | 30 | 2 | Q4XT96_PLACH | Q4xt96 plasmodium |
| 378 | 24 | 25.5 | 30 | 2 | Q4Y4P6_PLACH | Q4y4p6 plasmodium |
| 379 | 24 | 25.5 | 30 | 2 | Q4Z577_PLABE | Q4z577 plasmodium |
| 380 | 24 | 25.5 | 30 | 2 | Q3ACN1_CARHZ | Q3acn1 carboxydoth |
| 381 | 24 | 25.5 | 30 | 2 | Q3DPB2_STRAG | Q3dpb2 streptococc |
| 382 | 24 | 25.5 | 30 | 2 | Q44EF2_CHRSL | Q44ef2 chromohalob |
| 383 | 24 | 25.5 | 30 | 2 | Q4MSY5_BACCE | Q4msy5 bacillus ce |
| 384 | 24 | 25.5 | 30 | 2 | Q314V3_DESDG | Q314v3 desulfovibr |
| 385 | 24 | 25.5 | 30 | 2 | Q7MVC5_PORGI | Q7mvc5 porphyromon |
| 386 | 24 | 25.5 | 30 | 2 | Q8EH33_SHEON | Q8eh33 shewanella |
| 387 | 23.5 | 25.0 | 20 | 2 | Q9S8X5_SOYBN | Q9s8x5 glycine max |
| 388 | 23.5 | 25.0 | 22 | 2 | Q9URC2_PHACH | Q9urc2 phanerochae |
| 389 | 23.5 | 25.0 | 22 | 2 | Q9URC3_PHACH | Q9urc3 phanerochae |
| 390 | 23.5 | 25.0 | 23 | 2 | Q4XPS0_PLACH | Q4xps0 plasmodium |
| 391 | 23.5 | 25.0 | 26 | 2 | Q4YLV0_PLABE | Q4ylv0 plasmodium |
| 392 | 23.5 | 25.0 | 26 | 2 | Q9IDW1_9HIV2 | Q9idw1 human immun |
| 393 | 23.5 | 25.0 | 27 | 2 | Q4XG60_PLACH | Q4xg60 plasmodium |
| 394 | 23.5 | 25.0 | 28 | 2 | Q4YEQ5_PLABE | Q4yeq5 plasmodium |
| 395 | 23.5 | 25.0 | 28 | 2 | Q9XGE6_VICFA | Q9xge6 vicia faba |
| 396 | 23 | 24.5 | 8 | 2 | Q6EX61_9LAMI | Q6ex61 isodon hisp |
| 397 | 23 | 24.5 | 10 | 1 | SC46_TITCA | P84686 tityus camb |
| 398 | 23 | 24.5 | 10 | 2 | Q947R7_SOLTU | Q947r7 solanum tub |
| 399 | 23 | 24.5 | 12 | 2 | Q70Y67_9LAMI | Q70y67 prostanther |
| 400 | 23 | 24.5 | 12 | 2 | Q8GSB9_LOLPR | Q8gsb9 lolium pere |
| 401 | 23 | 24.5 | 14 | 2 | Q70Y96_9LAMI | Q70y96 ocimum amer |
| 402 | 23 | 24.5 | 14 | 2 | Q9ZRS3_ARATH | Q9zrs3 arabidopsis |
| 403 | 23 | 24.5 | 15 | 2 | Q88954_9POXV | Q88954 vaccinia vi |
| 404 | 23 | 24.5 | 16 | 1 | UVSX_BPT6 | Q06728 bacteriopha |
| 405 | 23 | 24.5 | 16 | 2 | Q51950_9ZZZZ | Q51950 plasmid pns |
| 406 | 23 | 24.5 | 16 | 2 | Q9R5E9_HAESO | Q9r5e9 haemophilus |
| 407 | 23 | 24.5 | 16 | 2 | Q5DUA1_STALE | Q5dua1 staphylococ |
| 408 | 23 | 24.5 | 17 | 1 | BOL4_MEGPE | P07495 megabombus |
| 409 | 23 | 24.5 | 17 | 2 | Q4YDE5_PLABE | Q4yde5 plasmodium |
| 410 | 23 | 24.5 | 17 | 2 | Q70Y62_MENSU | Q70y62 mentha suav |
| 411 | 23 | 24.5 | 17 | 2 | Q9T2H6_SPIOL | Q9t2h6 spinacia ol |
| 412 | 23 | 24.5 | 17 | 2 | Q712C7_RHIME | Q712c7 rhizobium m |
| 413 | 23 | 24.5 | 18 | 2 | Q7SCI4_NEUCR | Q7sci4 neurospora |
| 414 | 23 | 24.5 | 18 | 2 | Q4XSK3_PLACH | Q4xsk3 plasmodium |
| 415 | 23 | 24.5 | 18 | 2 | Q6ZYV2_9CARY | Q6zyv2 silene oste |
| 416 | 23 | 24.5 | 19 | 2 | Q45SP2_CLODI | Q45sp2 clostridium |
| 417 | 23 | 24.5 | 20 | 1 | JHBP_BOMMO | P81627 bombyx mori |
| 418 | 23 | 24.5 | 20 | 1 | NF03_NAEFO | P83898 naegleria f |
| 419 | 23 | 24.5 | 20 | 2 | Q7SAL6_NEUCR | Q7sal6 neurospora |
| 420 | 23 | 24.5 | 21 | 2 | Q4XF50_PLACH | Q4xf50 plasmodium |
| 421 | 23 | 24.5 | 21 | 2 | Q4Y571_PLACH | Q4y571 plasmodium |
| 422 | 23 | 24.5 | 21 | 2 | Q7RBF8_PLAYO | Q7rbf8 plasmodium |
| 423 | 23 | 24.5 | 21 | 2 | Q9ESX0_MOUSE | Q9esx0 mus musculu |
| 424 | 23 | 24.5 | 21 | 2 | O11791_9HIV1 | O11791 human immun |
| 425 | 23 | 24.5 | 21 | 2 | O11803_9HIV1 | O11803 human immun |
| 426 | 23 | 24.5 | 21 | 2 | O11804_9HIV1 | O11804 human immun |
| 427 | 23 | 24.5 | 21 | 2 | O11806_9HIV1 | O11806 human immun |
| 428 | 23 | 24.5 | 21 | 2 | O11807_9HIV1 | O11807 human immun |
| 429 | 23 | 24.5 | 21 | 2 | O11812_9HIV1 | O11812 human immun |
| 430 | 23 | 24.5 | 21 | 2 | O11825_9HIV1 | O11825 human immun |
| 431 | 23 | 24.5 | 21 | 2 | O11826_9HIV1 | O11826 human immun |

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| 432 | 23 | 24.5 | 21 | 2 | O11827_9HIV1 | O11827 human immun |
| 433 | 23 | 24.5 | 21 | 2 | O11831_9HIV1 | O11831 human immun |
| 434 | 23 | 24.5 | 21 | 2 | O11838_9HIV1 | O11838 human immun |
| 435 | 23 | 24.5 | 22 | 1 | UVSX_BPT2 | Q06727 bacteriopha |
| 436 | 23 | 24.5 | 22 | 2 | Q9UEY3_HUMAN | Q9uey3 homo sapien |
| 437 | 23 | 24.5 | 22 | 2 | Q4XUD0_PLACH | Q4xud0 plasmodium |
| 438 | 23 | 24.5 | 23 | 2 | Q4XTG0_PLACH | Q4xtg0 plasmodium |
| 439 | 23 | 24.5 | 23 | 2 | Q4Z0X5_PLABE | Q4z0x5 plasmodium |
| 440 | 23 | 24.5 | 23 | 2 | Q9XZW1_9CAEN | Q9xzw1 littorina a |
| 441 | 23 | 24.5 | 23 | 2 | Q9XZW4_LITLI | Q9xzw4 littorina l |
| 442 | 23 | 24.5 | 23 | 2 | Q9XZZ7_9CAEN | Q9xzz7 littorina s |
| 443 | 23 | 24.5 | 23 | 2 | Q9Y003_9CAEN | Q9y003 melarhaphe |
| 444 | 23 | 24.5 | 23 | 2 | Q68983_9ALPH | Q68983 suid herpes |
| 445 | 23 | 24.5 | 23 | 2 | Q98YK6_9HIV1 | Q98yk6 human immun |
| 446 | 23 | 24.5 | 24 | 2 | Q4XJG7_PLACH | Q4xjg7 plasmodium |
| 447 | 23 | 24.5 | 24 | 2 | Q4XV06_PLACH | Q4xv06 plasmodium |
| 448 | 23 | 24.5 | 24 | 2 | Q4YMW5_PLABE | Q4ymw5 plasmodium |
| 449 | 23 | 24.5 | 24 | 2 | Q4Z471_PLABE | Q4z471 plasmodium |
| 450 | 23 | 24.5 | 24 | 2 | Q29403_SHEEP | Q29403 ovis aries |
| 451 | 23 | 24.5 | 24 | 2 | Q6ZZ53_9CARY | Q6zz53 silene coel |
| 452 | 23 | 24.5 | 24 | 2 | Q9K8M1_BACHD | Q9k8m1 bacillus ha |
| 453 | 23 | 24.5 | 25 | 2 | Q4YA76_PLABE | Q4ya76 plasmodium |
| 454 | 23 | 24.5 | 25 | 2 | Q4YTS4_PLABE | Q4yts4 plasmodium |
| 455 | 23 | 24.5 | 25 | 2 | O77602_PAPAN | O77602 papio anubi |
| 456 | 23 | 24.5 | 25 | 2 | O77603_THEGE | O77603 theropithec |
| 457 | 23 | 24.5 | 25 | 2 | O77604_MACMU | O77604 macaca mula |
| 458 | 23 | 24.5 | 25 | 2 | O77605_MANLE | O77605 mandrillus |
| 459 | 23 | 24.5 | 25 | 2 | O77606_MANSP | O77606 mandrillus |
| 460 | 23 | 24.5 | 25 | 2 | O77607_LOPAT | O77607 lophocebus |
| 461 | 23 | 24.5 | 25 | 2 | O77827_LOPAA | O77827 lophocebus |
| 462 | 23 | 24.5 | 25 | 2 | O77828_CERTO | O77828 cercocebus |
| 463 | 23 | 24.5 | 25 | 2 | O77829_CERGC | O77829 cercocebus |
| 464 | 23 | 24.5 | 25 | 2 | O77831_CERMI | O77831 cercopithec |
| 465 | 23 | 24.5 | 25 | 2 | O77832_CERAE | O77832 cercopithec |
| 466 | 23 | 24.5 | 25 | 2 | Q7M156_BACTU | Q7m156 bacillus th |
| 467 | 23 | 24.5 | 25 | 2 | Q53I74_RAT | Q53i74 rattus norv |
| 468 | 23 | 24.5 | 25 | 2 | Q6SWG7_HCMV | Q6swg7 human cytom |
| 469 | 23 | 24.5 | 25 | 2 | Q56CD0_9HIV1 | Q56cd0 human immun |
| 470 | 23 | 24.5 | 25 | 2 | Q56CF6_9HIV1 | Q56cf6 human immun |
| 471 | 23 | 24.5 | 25 | 2 | Q56CF7_9HIV1 | Q56cf7 human immun |
| 472 | 23 | 24.5 | 25 | 2 | Q9DU23_9HIV1 | Q9du23 human immun |
| 473 | 23 | 24.5 | 26 | 1 | RL16_BACST | P23310 bacillus st |
| 474 | 23 | 24.5 | 26 | 2 | Q5ZQW9_9CAUD | Q5zqw9 bacteriopha |
| 475 | 23 | 24.5 | 26 | 2 | Q9QV79_9MURI | Q9qv79 rattus sp. |
| 476 | 23 | 24.5 | 26 | 2 | Q85461_9RETR | Q85461 avian myelo |
| 477 | 23 | 24.5 | 27 | 2 | Q7Z2G0_HUMAN | Q7z2g0 homo sapien |
| 478 | 23 | 24.5 | 27 | 2 | Q4Y431_PLACH | Q4y431 plasmodium |
| 479 | 23 | 24.5 | 27 | 2 | Q4YFL7_PLABE | Q4yfl7 plasmodium |
| 480 | 23 | 24.5 | 27 | 2 | Q4YZ78_PLABE | Q4yz78 plasmodium |
| 481 | 23 | 24.5 | 27 | 2 | Q9TM43_CYACA | Q9tm43 cyanidium c |
| 482 | 23 | 24.5 | 28 | 2 | Q7SAK0_NEUCR | Q7sak0 neurospora |
| 483 | 23 | 24.5 | 28 | 2 | Q4YFV6_PLABE | Q4yfv6 plasmodium |
| 484 | 23 | 24.5 | 28 | 2 | Q45QJ8_RAT | Q45qj8 rattus norv |
| 485 | 23 | 24.5 | 29 | 2 | O35358_RAT | O35358 rattus norv |
| 486 | 23 | 24.5 | 29 | 2 | P97599_RAT | P97599 rattus norv |
| 487 | 23 | 24.5 | 29 | 2 | Q9WVC4_MOUSE | Q9wvc4 mus musculu |
| 488 | 23 | 24.5 | 29 | 2 | Q90817_CHICK | Q90817 gallus gall |
| 489 | 23 | 24.5 | 30 | 2 | Q4XZM1_PLACH | Q4xzm1 plasmodium |
| 490 | 23 | 24.5 | 30 | 2 | Q4YDJ7_PLABE | Q4ydj7 plasmodium |
| 491 | 23 | 24.5 | 30 | 2 | Q7RHK1_PLAYO | Q7rhk1 plasmodium |
| 492 | 23 | 24.5 | 30 | 2 | Q7RHQ9_PLAYO | Q7rhq9 plasmodium |

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|---|---|---|---|---|---|---|
| 493 | 23 | 24.5 | 30 | 2 | Q03618_STRHY | Q03618 streptomyce |
| 494 | 23 | 24.5 | 30 | 2 | Q47Z49_COLP3 | Q47z49 colwellia p |
| 495 | 23 | 24.5 | 30 | 2 | Q4MGH8_BACCE | Q4mgh8 bacillus ce |
| 496 | 23 | 24.5 | 30 | 2 | Q9R5A3_9PSED | Q9r5a3 pseudomonas |
| 497 | 23 | 24.5 | 30 | 2 | Q57BN2_BRUAB | Q57bn2 brucella ab |
| 498 | 23 | 24.5 | 30 | 2 | Q72B97_DESVH | Q72b97 desulfovibr |
| 499 | 23 | 24.5 | 30 | 2 | Q7VKB9_HAEDU | Q7vkb9 haemophilus |
| 500 | 23 | 24.5 | 30 | 2 | Q8FZ53_BRUSU | Q8fz53 brucella su |
| 501 | 23 | 24.5 | 30 | 2 | Q2YRK9_BRUA2 | Q2yrk9 brucella ab |
| 502 | 23 | 24.5 | 30 | 2 | Q4T6V6_TETNG | Q4t6v6 tetraodon n |
| 503 | 23 | 24.5 | 30 | 2 | Q9W7N3_MORSA | Q9w7n3 morone saxa |
| 504 | 22.5 | 23.9 | 23 | 2 | Q4XJB4_PLACH | Q4xjb4 plasmodium |
| 505 | 22.5 | 23.9 | 25 | 2 | Q4RAH1_TETNG | Q4rah1 tetraodon n |
| 506 | 22.5 | 23.9 | 26 | 2 | Q4YXA8_PLABE | Q4yxa8 plasmodium |
| 507 | 22.5 | 23.9 | 30 | 2 | Q9TWM4_MANSE | Q9twm4 manduca sex |
| 508 | 22.5 | 23.9 | 30 | 2 | Q8SMQ5_9AQUA | Q8smq5 ilex repand |
| 509 | 22 | 23.4 | 9 | 2 | Q67AQ7_HUMAN | Q67aq7 homo sapien |
| 510 | 22 | 23.4 | 9 | 2 | Q7EXP6_HORVD | Q7exp6 hordeum vul |
| 511 | 22 | 23.4 | 9 | 2 | Q9FEC0_HORVU | Q9fec0 hordeum vul |
| 512 | 22 | 23.4 | 10 | 2 | Q8GZC8_HORVU | Q8gzc8 hordeum vul |
| 513 | 22 | 23.4 | 13 | 1 | SODM_ARTDA | P83289 arthrobotry |
| 514 | 22 | 23.4 | 14 | 1 | PLYB1_POLPI | P84388 polybia pau |
| 515 | 22 | 23.4 | 14 | 2 | Q7M0Q6_9THEM | Q7m0q6 thermotoga |
| 516 | 22 | 23.4 | 15 | 2 | Q56IZ1_9FLAV | Q56iz1 tick-borne |
| 517 | 22 | 23.4 | 15 | 2 | Q5R3U5_XENLA | Q5r3u5 xenopus lae |
| 518 | 22 | 23.4 | 16 | 2 | Q6JQ71_HBV | Q6jq71 hepatitis b |
| 519 | 22 | 23.4 | 17 | 1 | PATS_ANASP | O52748 anabaena sp |
| 520 | 22 | 23.4 | 17 | 2 | Q7RQU2_PLAYO | Q7rqu2 plasmodium |
| 521 | 22 | 23.4 | 17 | 2 | Q3V3P2_MOUSE | Q3v3p2 mus musculu |
| 522 | 22 | 23.4 | 17 | 2 | Q811C1_MOUSE | Q811c1 mus musculu |
| 523 | 22 | 23.4 | 17 | 2 | Q5R3U2_XENLA | Q5r3u2 xenopus lae |
| 524 | 22 | 23.4 | 17 | 2 | Q7T080_9AVES | Q7t080 anser anser |
| 525 | 22 | 23.4 | 17 | 2 | Q7T081_ANAPL | Q7t081 anas platyr |
| 526 | 22 | 23.4 | 18 | 2 | Q8RU82_MAIZE | Q8ru82 zea mays (m |
| 527 | 22 | 23.4 | 19 | 2 | Q4Z5V1_PLABE | Q4z5v1 plasmodium |
| 528 | 22 | 23.4 | 19 | 2 | Q9BGH0_PIG | Q9bgh0 sus scrofa |
| 529 | 22 | 23.4 | 19 | 2 | Q38371_BPMS2 | Q38371 bacteriopha |
| 530 | 22 | 23.4 | 20 | 1 | GUAA_LACSN | P83540 lactobacill |
| 531 | 22 | 23.4 | 20 | 2 | Q9TWN5_THESE | Q9twn5 theileria s |
| 532 | 22 | 23.4 | 20 | 2 | Q9S8K2_SOLTU | Q9s8k2 solanum tub |
| 533 | 22 | 23.4 | 20 | 2 | Q7M195_THEAQ | Q7m195 thermus aqu |
| 534 | 22 | 23.4 | 20 | 2 | Q9QUZ1_9MURI | Q9quz1 rattus sp. |
| 535 | 22 | 23.4 | 21 | 1 | OMP44_PASHA | P80228 pasteurella |
| 536 | 22 | 23.4 | 21 | 1 | THAN_PODMA | P55788 podisus mac |
| 537 | 22 | 23.4 | 21 | 2 | Q4XNE6_PLACH | Q4xne6 plasmodium |
| 538 | 22 | 23.4 | 21 | 2 | Q4XX24_PLACH | Q4xx24 plasmodium |
| 539 | 22 | 23.4 | 21 | 2 | Q4Y631_PLACH | Q4y631 plasmodium |
| 540 | 22 | 23.4 | 21 | 2 | Q4Y8P3_PLACH | Q4y8p3 plasmodium |
| 541 | 22 | 23.4 | 21 | 2 | Q4Y9Z3_PLABE | Q4y9z3 plasmodium |
| 542 | 22 | 23.4 | 21 | 2 | Q9ZYB7_9HYME | Q9zyb7 spinaria sp |
| 543 | 22 | 23.4 | 21 | 2 | Q93CI4_ECOLI | Q93ci4 escherichia |
| 544 | 22 | 23.4 | 22 | 2 | Q4XAK9_PLACH | Q4xak9 plasmodium |
| 545 | 22 | 23.4 | 22 | 2 | Q9IAV6_9PASS | Q9iav6 acanthiza n |
| 546 | 22 | 23.4 | 22 | 2 | Q9IAV7_9PASS | Q9iav7 acanthiza l |
| 547 | 22 | 23.4 | 22 | 2 | Q9IAV8_9PASS | Q9iav8 acanthiza r |
| 548 | 22 | 23.4 | 22 | 2 | Q9IAV9_9PASS | Q9iav9 acanthiza u |
| 549 | 22 | 23.4 | 22 | 2 | Q9IAW0_9PASS | Q9iaw0 acanthiza r |
| 550 | 22 | 23.4 | 22 | 2 | Q9IAW1_9PASS | Q9iaw1 acanthiza i |
| 551 | 22 | 23.4 | 22 | 2 | Q9IAW2_9PASS | Q9iaw2 acanthiza i |
| 552 | 22 | 23.4 | 22 | 2 | Q9IAW3_9PASS | Q9iaw3 acanthiza p |
| 553 | 22 | 23.4 | 22 | 2 | Q9IAW4_ACAKA | Q9iaw4 acanthiza k |

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| 554 | 22 | 23.4 | 22 | 2 | Q9IAW5_9PASS | Q9iaw5 acanthiza e |
| 555 | 22 | 23.4 | 22 | 2 | Q9IAW6_9PASS | Q9iaw6 acanthiza c |
| 556 | 22 | 23.4 | 22 | 2 | Q9IAW7_9PASS | Q9iaw7 acanthiza a |
| 557 | 22 | 23.4 | 22 | 2 | Q9IAW8_9PASS | Q9iaw8 smicrornis |
| 558 | 22 | 23.4 | 22 | 2 | Q9IAW9_9PASS | Q9iaw9 gerygone fu |
| 559 | 22 | 23.4 | 22 | 2 | Q9IAX0_9PASS | Q9iax0 aphelocepha |
| 560 | 22 | 23.4 | 22 | 2 | Q9IAX1_9PASS | Q9iax1 sericornis |
| 561 | 22 | 23.4 | 22 | 2 | Q8AEW5_9HIV1 | Q8aew5 human immun |
| 562 | 22 | 23.4 | 22 | 2 | Q8AEW9_9HIV1 | Q8aew9 human immun |
| 563 | 22 | 23.4 | 23 | 2 | Q4XXR5_PLACH | Q4xxr5 plasmodium |
| 564 | 22 | 23.4 | 23 | 2 | Q4YRL7_PLABE | Q4yrl7 plasmodium |
| 565 | 22 | 23.4 | 23 | 2 | Q7RSU3_PLAYO | Q7rsu3 plasmodium |
| 566 | 22 | 23.4 | 23 | 2 | O18841_PIG | O18841 sus scrofa |
| 567 | 22 | 23.4 | 23 | 2 | Q4JQP8_PIG | Q4jqp8 sus scrofa |
| 568 | 22 | 23.4 | 23 | 2 | Q9T354_MACSY | Q9t354 macaca sylv |
| 569 | 22 | 23.4 | 23 | 2 | Q3KU33_STRCR | Q3ku33 streptococc |
| 570 | 22 | 23.4 | 23 | 2 | Q47WG5_COLP3 | Q47wg5 colwellia p |
| 571 | 22 | 23.4 | 23 | 2 | Q57162_ENTFA | Q57162 enterococcu |
| 572 | 22 | 23.4 | 23 | 2 | Q5PFC9_SALPA | Q5pfc9 salmonella |
| 573 | 22 | 23.4 | 23 | 2 | Q8E018_STRA5 | Q8e018 streptococc |
| 574 | 22 | 23.4 | 23 | 2 | Q8Z974_SALTI | Q8z974 salmonella |
| 575 | 22 | 23.4 | 24 | 2 | Q4XYM2_PLACH | Q4xym2 plasmodium |
| 576 | 22 | 23.4 | 24 | 2 | Q4YB25_PLABE | Q4yb25 plasmodium |
| 577 | 22 | 23.4 | 24 | 2 | Q4Z5N0_PLABE | Q4z5n0 plasmodium |
| 578 | 22 | 23.4 | 24 | 2 | Q94370_CAEEL | Q94370 caenorhabdi |
| 579 | 22 | 23.4 | 24 | 2 | Q9TRE8_BOVIN | Q9tre8 bos taurus |
| 580 | 22 | 23.4 | 25 | 1 | CPI2_SOLTU | P24744 solanum tub |
| 581 | 22 | 23.4 | 25 | 1 | HCY3_MAISQ | P82304 maia squina |
| 582 | 22 | 23.4 | 25 | 1 | RL29_BREVE | Q9r4p0 brevundimon |
| 583 | 22 | 23.4 | 25 | 1 | TFDC2_COMAC | P83116 comamonas a |
| 584 | 22 | 23.4 | 25 | 2 | Q4X3H5_PLACH | Q4x3h5 plasmodium |
| 585 | 22 | 23.4 | 25 | 2 | Q4XCD1_PLACH | Q4xcd1 plasmodium |
| 586 | 22 | 23.4 | 25 | 2 | Q4Y5T2_PLACH | Q4y5t2 plasmodium |
| 587 | 22 | 23.4 | 25 | 2 | Q4Y9R3_PLABE | Q4y9r3 plasmodium |
| 588 | 22 | 23.4 | 25 | 2 | Q7R8K6_PLAYO | Q7r8k6 plasmodium |
| 589 | 22 | 23.4 | 25 | 2 | Q7RAC5_PLAYO | Q7rac5 plasmodium |
| 590 | 22 | 23.4 | 25 | 2 | Q7RJP0_PLAYO | Q7rjp0 plasmodium |
| 591 | 22 | 23.4 | 25 | 2 | Q9BM55_9BIVA | Q9bm55 chione canc |
| 592 | 22 | 23.4 | 25 | 2 | Q6JDJ8_CANFA | Q6jdj8 canis famil |
| 593 | 22 | 23.4 | 25 | 2 | Q40972_PINRA | Q40972 pinus radia |
| 594 | 22 | 23.4 | 25 | 2 | Q40973_PINRA | Q40973 pinus radia |
| 595 | 22 | 23.4 | 25 | 2 | Q56C54_9HIV1 | Q56c54 human immun |
| 596 | 22 | 23.4 | 25 | 2 | Q56C55_9HIV1 | Q56c55 human immun |
| 597 | 22 | 23.4 | 25 | 2 | Q56C56_9HIV1 | Q56c56 human immun |
| 598 | 22 | 23.4 | 25 | 2 | Q56C57_9HIV1 | Q56c57 human immun |
| 599 | 22 | 23.4 | 25 | 2 | Q56C58_9HIV1 | Q56c58 human immun |
| 600 | 22 | 23.4 | 25 | 2 | Q56C59_9HIV1 | Q56c59 human immun |
| 601 | 22 | 23.4 | 25 | 2 | Q56C60_9HIV1 | Q56c60 human immun |
| 602 | 22 | 23.4 | 25 | 2 | Q56C61_9HIV1 | Q56c61 human immun |
| 603 | 22 | 23.4 | 25 | 2 | Q56C62_9HIV1 | Q56c62 human immun |
| 604 | 22 | 23.4 | 25 | 2 | Q56C63_9HIV1 | Q56c63 human immun |
| 605 | 22 | 23.4 | 25 | 2 | Q56C65_9HIV1 | Q56c65 human immun |
| 606 | 22 | 23.4 | 25 | 2 | Q56C66_9HIV1 | Q56c66 human immun |
| 607 | 22 | 23.4 | 25 | 2 | Q56C67_9HIV1 | Q56c67 human immun |
| 608 | 22 | 23.4 | 25 | 2 | Q56C69_9HIV1 | Q56c69 human immun |
| 609 | 22 | 23.4 | 25 | 2 | Q56C70_9HIV1 | Q56c70 human immun |
| 610 | 22 | 23.4 | 25 | 2 | Q56C71_9HIV1 | Q56c71 human immun |
| 611 | 22 | 23.4 | 25 | 2 | Q56C72_9HIV1 | Q56c72 human immun |
| 612 | 22 | 23.4 | 25 | 2 | Q56C73_9HIV1 | Q56c73 human immun |
| 613 | 22 | 23.4 | 25 | 2 | Q56C74_9HIV1 | Q56c74 human immun |
| 614 | 22 | 23.4 | 25 | 2 | Q56C75_9HIV1 | Q56c75 human immun |

10/715,810

RESULT 3
ADZ69738
ID ADZ69738 standard; peptide; 20 AA.
XX
AC ADZ69738;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:13.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Example 1; SEQ ID NO 13; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 20 AA;

aa 785-803

Query Match 89.2%; Score 91; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

RESULT 4
ADZ69808
ID  ADZ69808 standard; peptide; 20 AA.
XX
AC  ADZ69808;
XX
DT  28-JUL-2005  (first entry)
XX
DE  Botulinum toxin type A peptide SEQ ID NO:83.
XX
KW  toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW  autonomic nervous system disease; pain; neuromuscular disease;
KW  cervical dystonia; migraine.
XX
OS  Clostridium botulinum.
XX
PN  US2005106182-A1.
XX
PD  19-MAY-2005.
XX
PF  17-NOV-2003; 2003US-00715810.
XX
PR  17-NOV-2003; 2003US-00715810.
XX
PA  (LISS/) LI S.
PA  (AOKI/) AOKI K R.
XX
PI  Li S,  Aoki KR;
XX
DR  WPI; 2005-365766/37.
XX
PT  Treating botulinum toxin intoxication in a mammal, comprises
PT  administering a rescue agent comprising an inactive botulinum toxin and a
PT  modified nontoxic nonhemagglutinin to a mammal.
XX
PS  Disclosure; SEQ ID NO 83; 61pp; English.
XX
CC  The invention relates to a method (M1) for treating botulinum toxin
CC  intoxication in a mammal. (M1) comprises administering at least one
CC  rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC  being glycosylated, having reduced antigenicity, and being inactive; (2)
CC  making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC  in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC  comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC  non-Clostridium botulinum cell (III) comprising a vector operatively
CC  harboring a nucleotide sequence encoding a single chain botulinum toxin
CC  and a vector operatively harboring nucleotide sequence encoding a
CC  nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC  condition, an autonomic nervous system disorder and/or pain, which
CC  involves administering (II) to the mammal in need of the toxins. (II) is
CC  also useful for the treatment of neuromuscular disorders, cervical
CC  dystonia and migraine. The present sequence represents a Clostridium
CC  botulinum toxin type A peptide sequence, which is used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 20 AA;

  Query Match             89.2%;  Score 91;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

qa 785-803

```
Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

RESULT 5
ADZ69753
ID  ADZ69753 standard; peptide; 20 AA.
XX
AC  ADZ69753;
XX
DT  28-JUL-2005  (first entry)
XX
DE  Botulinum toxin type A peptide SEQ ID NO:28.
XX
KW  toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW  autonomic nervous system disease; pain; neuromuscular disease;
KW  cervical dystonia; migraine.
XX
OS  Clostridium botulinum.
XX
PN  US2005106182-A1.
XX
PD  19-MAY-2005.
XX
PF  17-NOV-2003; 2003US-00715810.
XX
PR  17-NOV-2003; 2003US-00715810.
XX
PA  (LISS/) LI S.
PA  (AOKI/) AOKI K R.
XX
PI  Li S,  Aoki KR;
XX
DR  WPI; 2005-365766/37.
XX
PT  Treating botulinum toxin intoxication in a mammal, comprises
PT  administering a rescue agent comprising an inactive botulinum toxin and a
PT  modified nontoxic nonhemagglutinin to a mammal.
XX
PS  Example 1; SEQ ID NO 28; 61pp; English.
XX
CC  The invention relates to a method (M1) for treating botulinum toxin
CC  intoxication in a mammal. (M1) comprises administering at least one
CC  rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC  being glycosylated, having reduced antigenicity, and being inactive; (2)
CC  making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC  in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC  comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC  non-Clostridium botulinum cell (III) comprising a vector operatively
CC  harboring a nucleotide sequence encoding a single chain botulinum toxin
CC  and a vector operatively harboring nucleotide sequence encoding a
CC  nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC  condition, an autonomic nervous system disorder and/or pain, which
CC  involves administering (II) to the mammal in need of the toxins. (II) is
CC  also useful for the treatment of neuromuscular disorders, cervical
CC  dystonia and migraine. The present sequence represents a Clostridium
CC  botulinum toxin type A peptide sequence, which is used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 20 AA;

  Query Match             89.2%;  Score 91;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

ca 785-803

```
Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

ADJ82841
ID ADJ82841 standard; peptide; 14 AA.
XX
AC ADJ82841;
XX
DT 06-MAY-2004 (first entry)
XX
DE Tetanus Tet(639)V epitope for fusion peptide vaccine.
XX
KW immunostimulant; vaccine; cytomegalovirus; fusion peptide;
KW T helper epitope; CTL epitope; PADRE; tetanus epitope; DNA adjuvant;
KW immune system.
XX
OS Clostridium tetani.
OS Unidentified.
XX
PN WO2004000873-A2.
XX
PD 31-DEC-2003.
XX
PF 25-JUN-2003; 2003WO-US019848.
XX
PR 25-JUN-2002; 2002US-0391088P.
XX
PA (CITY ) CITY OF HOPE.
XX
PI Diamond DJ;
XX
DR WPI; 2004-082471/08.
XX
PT New cytomegalovirus (CMV) vaccine comprising a fusion peptide composed of
PT a T helper epitope fused to a CMV CTL epitope peptide, useful in
PT manufacturing a medicament for modifying the immune system of a mammal
PT against CMV.
XX
PS Disclosure; SEQ ID NO 4; 52pp; English.
XX
CC The invention relates to a cytomegalovirus vaccine comprising a fusion
CC peptide composed of a T helper epitope fused to a CMV CTL epitope
CC peptide. The T helper epitope is PADRE or a tetanus epitope selected from
CC tetanus heavy chain (590-603), tetanus heavy chain (615-629), tetanus
CC heavy chain (639-652), tetanus heavy chain (830-843), and tetanus heavy
CC chain (947-967). The CMV pp65 CTL epitope peptide is selected from
CC pp65(13-24), pp65(186-196), pp65(188-195), pp65(265-275), pp65(363-373),
CC pp65(369-379), pp65(367-379), pp65(495-503), and pp65(417-426),
CC preferably pp65(495-503). The vaccine may further comprise a DNA
CC adjuvant. The vaccine is useful in the manufacture of a medicament for
CC modifying the immune system of a mammal against CMV. This sequence
CC corresponds to the tetanus epitope Tet(639)V used in the vaccine of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 56.6%; Score 56; DB 8; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.048;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 IIPYIGPALNI 13
              |:|||||||||
Db          4 IVPYIGPALNI 14
```

ADJ82841
ID ADJ82841 standard; peptide; 14 AA.
XX
AC ADJ82841;
XX
DT 06-MAY-2004 (first entry)
XX
DE Tetanus Tet(639)V epitope for fusion peptide vaccine.
XX
KW immunostimulant; vaccine; cytomegalovirus; fusion peptide;
KW T helper epitope; CTL epitope; PADRE; tetanus epitope; DNA adjuvant;
KW immune system.
XX
OS Clostridium tetani.
OS Unidentified.
XX
PN WO2004000873-A2.
XX
PD 31-DEC-2003.
XX
PF 25-JUN-2003; 2003WO-US019848.
XX
PR 25-JUN-2002; 2002US-0391088P.
XX
PA (CITY ) CITY OF HOPE.
XX
PI Diamond DJ;
XX
DR WPI; 2004-082471/08.
XX
PT New cytomegalovirus (CMV) vaccine comprising a fusion peptide composed of
PT a T helper epitope fused to a CMV CTL epitope peptide, useful in
PT manufacturing a medicament for modifying the immune system of a mammal
PT against CMV.
XX
PS Disclosure; SEQ ID NO 4; 52pp; English.
XX
CC The invention relates to a cytomegalovirus vaccine comprising a fusion
CC peptide composed of a T helper epitope fused to a CMV CTL epitope
CC peptide. The T helper epitope is PADRE or a tetanus epitope selected from
CC tetanus heavy chain (590-603), tetanus heavy chain (615-629), tetanus
CC heavy chain (639-652), tetanus heavy chain (830-843), and tetanus heavy
CC chain (947-967). The CMV pp65 CTL epitope peptide is selected from
CC pp65(13-24), pp65(186-196), pp65(188-195), pp65(265-275), pp65(363-373),
CC pp65(369-379), pp65(367-379), pp65(495-503), and pp65(417-426),
CC preferably pp65(495-503). The vaccine may further comprise a DNA
CC adjuvant. The vaccine is useful in the manufacture of a medicament for
CC modifying the immune system of a mammal against CMV. This sequence
CC corresponds to the tetanus epitope Tet(639)V used in the vaccine of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 56.6%; Score 56; DB 8; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.048;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IIPYIGPALNI 13
:|||||||||
Db 4 IVPYIGPALNI 14

RESULT 5
ADZ69794
ID ADZ69794 standard; peptide; 8 AA.
XX
AC ADZ69794;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:69.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 69; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 8 AA;

Query Match 44.8%; Score 47; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

547-565

```
Qy          2 YTMFHYLR 9
              ||||||||
Db          1 YTMFHYLR 8
```

ADZ69798
ID ADZ69798 standard; peptide; 30 AA.
XX
AC ADZ69798;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:73.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 73; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 30 AA;

Query Match 58.0%; Score 58; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATEAAMFLGWV 19

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                ||||||||||
Db          1 ATEAAMFLGWV 11
```

```
 Sequence 74, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 627-649)
US-10-715-810-74

  Query Match             100.0%;  Score 99;  DB 5;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-09;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TIIIPYIGPALNIGNMLYK 19
              ||||||||||||||||||
Db          5 TIIIPYIGPALNIGNMLYK 23
```

RESULT 4
ADZ69803
ID ADZ69803 standard; peptide; 9 AA.
XX
AC ADZ69803;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:78.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 78; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 43.9%; Score 43; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 VNTQIDLIR 15
              |||||||||
Db          1 VNTQIDLIR 9
```

715-733

RESULT 20
ADZ69802
ID  ADZ69802 standard; peptide; 9 AA.
XX
AC  ADZ69802;
XX
DT  28-JUL-2005  (first entry)
XX
DE  Botulinum toxin type A peptide SEQ ID NO:77.
XX
KW  toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW  autonomic nervous system disease; pain; neuromuscular disease;
KW  cervical dystonia; migraine.
XX
OS  Clostridium botulinum.
XX
PN  US2005106182-A1.
XX
PD  19-MAY-2005.
XX
PF  17-NOV-2003; 2003US-00715810.
XX
PR  17-NOV-2003; 2003US-00715810.
XX
PA  (LISS/) LI S.
PA  (AOKI/) AOKI K R.
XX
PI  Li S,  Aoki KR;
XX
DR  WPI; 2005-365766/37.
XX
PT  Treating botulinum toxin intoxication in a mammal, comprises
PT  administering a rescue agent comprising an inactive botulinum toxin and a
PT  modified nontoxic nonhemagglutinin to a mammal.
XX
PS  Disclosure; SEQ ID NO 77; 61pp; English.
XX
CC  The invention relates to a method (M1) for treating botulinum toxin
CC  intoxication in a mammal. (M1) comprises administering at least one
CC  rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC  being glycosylated, having reduced antigenicity, and being inactive; (2)
CC  making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC  in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC  comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC  non-Clostridium botulinum cell (III) comprising a vector operatively
CC  harboring a nucleotide sequence encoding a single chain botulinum toxin
CC  and a vector operatively harboring nucleotide sequence encoding a
CC  nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC  condition, an autonomic nervous system disorder and/or pain, which
CC  involves administering (II) to the mammal in need of the toxins. (II) is
CC  also useful for the treatment of neuromuscular disorders, cervical
CC  dystonia and migraine. The present sequence represents a Clostridium
CC  botulinum toxin type A peptide sequence, which is used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 9 AA;

  Query Match             35.7%;  Score 35;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```
Qy          1 TNWLAK 6
              ||||||
Db          4 TNWLAK 9
```

RESULT 3
ADZ69805
ID  ADZ69805 standard; peptide; 15 AA.
XX
AC  ADZ69805;
XX
DT  28-JUL-2005  (first entry)
XX
DE  Botulinum toxin type A peptide SEQ ID NO:80.
XX
KW  toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW  autonomic nervous system disease; pain; neuromuscular disease;
KW  cervical dystonia; migraine.
XX
OS  Clostridium botulinum.
XX
PN  US2005106182-A1.
XX
PD  19-MAY-2005.
XX
PF  17-NOV-2003; 2003US-00715810.
XX
PR  17-NOV-2003; 2003US-00715810.
XX
PA  (LISS/) LI S.
PA  (AOKI/) AOKI K R.
XX
PI  Li S,  Aoki KR;
XX
DR  WPI; 2005-365766/37.
XX
PT  Treating botulinum toxin intoxication in a mammal, comprises
PT  administering a rescue agent comprising an inactive botulinum toxin and a
PT  modified nontoxic nonhemagglutinin to a mammal.
XX
PS  Disclosure; SEQ ID NO 80; 61pp; English.
XX
CC  The invention relates to a method (M1) for treating botulinum toxin
CC  intoxication in a mammal. (M1) comprises administering at least one
CC  rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC  being glycosylated, having reduced antigenicity, and being inactive; (2)
CC  making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC  in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC  comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC  non-Clostridium botulinum cell (III) comprising a vector operatively
CC  harboring a nucleotide sequence encoding a single chain botulinum toxin
CC  and a vector operatively harboring nucleotide sequence encoding a
CC  nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC  condition, an autonomic nervous system disorder and/or pain, which
CC  involves administering (II) to the mammal in need of the toxins. (II) is
CC  also useful for the treatment of neuromuscular disorders, cervical
CC  dystonia and migraine. The present sequence represents a Clostridium
CC  botulinum toxin type A peptide sequence, which is used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 15 AA;

  Query Match             78.4%;  Score 80;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```
Qy          3 AIINYQYNQYTEEEK 17
              |||||||||||||||
Db          1 AIINYQYNQYTEEEK 15
```

RESULT 2
ADZ69820
ID  ADZ69820 standard; peptide; 19 AA.
XX
AC  ADZ69820;
XX
DT  28-JUL-2005  (first entry)
XX
DE  Botulinum toxin type A peptide SEQ ID NO:95.
XX
KW  toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW  autonomic nervous system disease; pain; neuromuscular disease;
KW  cervical dystonia; migraine.
XX
OS  Clostridium botulinum.
XX
PN  US2005106182-A1.
XX
PD  19-MAY-2005.
XX
PF  17-NOV-2003; 2003US-00715810.
XX
PR  17-NOV-2003; 2003US-00715810.
XX
PA  (LISS/) LI S.
PA  (AOKI/) AOKI K R.
XX
PI  Li S,  Aoki KR;
XX
DR  WPI; 2005-365766/37.
XX
PT  Treating botulinum toxin intoxication in a mammal, comprises
PT  administering a rescue agent comprising an inactive botulinum toxin and a
PT  modified nontoxic nonhemagglutinin to a mammal.
XX
PS  Disclosure; SEQ ID NO 95; 61pp; English.
XX
CC  The invention relates to a method (M1) for treating botulinum toxin
CC  intoxication in a mammal. (M1) comprises administering at least one
CC  rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC  being glycosylated, having reduced antigenicity, and being inactive; (2)
CC  making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC  in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC  comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC  non-Clostridium botulinum cell (III) comprising a vector operatively
CC  harboring a nucleotide sequence encoding a single chain botulinum toxin
CC  and a vector operatively harboring nucleotide sequence encoding a
CC  nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC  condition, an autonomic nervous system disorder and/or pain, which
CC  involves administering (II) to the mammal in need of the toxins. (II) is
CC  also useful for the treatment of neuromuscular disorders, cervical
CC  dystonia and migraine. The present sequence represents a Clostridium
CC  botulinum toxin type A peptide sequence, which is used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 19 AA;

ga 981-999

Query Match  75.5%;  Score 74;  DB 9;  Length 19;
Best Local Similarity  100.0%;  Pred. No. 0.00012;
Matches  14;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```
Qy          1 GEIIWTLQDTQEIK 14
              ||||||||||||||
Db          6 GEIIWTLQDTQEIK 19
```

```
RESULT 41
US-10-715-810-99
; Sequence 99, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 1035-1056)
US-10-715-810-99

  Query Match             28.6%;  Score 32;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NNIMFK 6
              ||||||
Db         17 NNIMFK 22
```

aa 1051-1069

RESULT 2
ADZ69830
ID ADZ69830 standard; peptide; 20 AA.
XX
AC ADZ69830;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:105.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 105; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 20 AA;

aa 275-1296

Query Match 93.1%; Score 121; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 TLGCSWEFIPVDDGWGERPL 22
              ||||||||||||||||||||
Db          1 TLGCSWEFIPVDDGWGERPL 20
```

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 13:45:45 ; Search time 57.1624 Seconds
(without alignments)
153.966 Million cell updates/sec

Title: US-10-821-669-1_COPY_673_691
Perfect score: 91
Sequence: 1 IPVLGTFALVSYIANKVLT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 526792

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 34 | 37.4 | 28 | 4 | [redacted] | Sequence 28518, A |

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:30:50 ; Search time 99.3 Seconds
(without alignments)
176.992 Million cell updates/sec

Title: US-10-821-669-1_COPY_589_607
Perfect score: 100
Sequence: 1 DYVKKVNKATEAAMFLGWV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 33 | 33.0 | 20 | 2 | Q9ZY85_BOMTE | Q9zy85 bombus terr |
| 2 | 33 | 33.0 | 30 | 2 | Q73RF8_TREDE | Q73rf8 treponema d |

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_491_509
Perfect score: 99
Sequence: 1 EENISLDLIQQYYLTFNFD 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 99 | 100.0 | 19 | 9 | ADW11044 | Adw11044 Clostridi |
| 2 | 99 | 100.0 | 27 | 9 | ADW11103 | Adw11103 Clostridi |
| 3 | 37 | 37.4 | 14 | 9 | ADV55232 | Adv55232 G protein |

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 107.179 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_1275_1296
Perfect score: 130
Sequence: 1 SRTLGCSWEFIPVDDGWGERPL 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 130 | 100.0 | 22 | 9 | ADW11100 | Adw11100 Clostridi |
| 2 | 121 | 93.1 | 20 | 9 | ADZ69830 | Adz69830 Botulinum |
| 3 | 70 | 53.8 | 20 | 2 | AAR47809 | Aar47809 Sequence |
| 4 | 70 | 53.8 | 21 | 2 | AAR04088 | Aar04088 The carbo |
| 5 | 70 | 53.8 | 21 | 2 | AAR47810 | Aar47810 Sequence |
| 6 | 45 | 34.6 | 19 | 5 | AAU85629 | Aau85629 Lung tumo |

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_1121_1139
Perfect score: 104
Sequence: 1 KYVDVNNVGIRGYMYLKGP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 104 | 100.0 | 19 | 9 | ADW11089 | Adw11089 Clostridi |

```
AAW11973
ID   AAW11973 standard; peptide; 8 AA.
XX
AC   AAW11973;
XX
DT   02-APR-1997  (first entry)
XX
DE   T-cell epitope #4 from tetanus toxoid.
XX
KW   T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
KW   HIV sf2; herpes simplex virus; antigen gD2; tetanus toxoid; vaccine; HSV;
KW   mammal; gp120; immune response; B-cell antigen.
XX
OS   Synthetic.
XX
PN   WO9518148-A1.
XX
PD   06-JUL-1995.
XX
PF   28-DEC-1993;   93WO-US011703.
XX
PR   28-DEC-1993;   93WO-US011703.
XX
PA   (CHIR-) CHIRON MIMOTOPES PTY LTD.
XX
PI   Geysen HM,  Rodda SJ;
XX
DR   WPI; 1995-246333/32.
XX
PT   T cell epitope peptide(s) - useful for detecting exposure of a subject to
PT   an antigen or pathogen, and in vaccines for birds and mammals.
XX
PS   Claim 1; Page 45; 57pp; English.
XX
CC   AAW11953-W11976 represent T-cell epitope peptides. T-cell epitopes (also
CC   known as T-cell determinants) are peptides (or regions of a protein)
CC   which bind to T-cell antigen receptors in conjugation with MHC proteins.
CC   These sequences were the most antigenic peptides obtained from pools of
CC   peptides created from the HIV sf2 gp120 (AAW11953-W11960), herpes simplex
CC   virus antigen gD2 (AAW11961-W11969), and tetanus toxoid (AAW11970-
CC   W11976). These sequences can be used in methods for detecting exposure of
CC   a mammal or bird to an antigen, and for increasing the number of T-cells
CC   specific for an antigen. The peptides can also be used in a method for
CC   determining T-cell epitopes specific for an antigen. These methods allow
CC   for the identification of T-cell determinants. The T-cell epitope
CC   peptides can be used in a vaccine for inducing an immune response in a
CC   bird or mammal. The vaccine also contains a B-cell antigen, preferably
CC   herpes simplex virus gD2 or HIV sf2 gp120 (see AAW11977), and a carrier
XX
SQ   Sequence 8 AA;

  Query Match             42.4%;  Score 42;  DB 2;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 2.1e+06;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPA 10
              |:||||||
Db          1 IVPYIGPA 8
```

96631-649

ID AAW05608 standard; peptide; 16 AA.
XX
AC AAW05608;
XX
DT 10-DEC-1996 (first entry)
XX
DE Tetanus toxin helper T cell epitope #5.
XX
KW Immunoglobulin; IgE; membrane protein; human; epsilon chain; hepatitis B;
KW membrane anchoring domain; helper T cell; surface antigen; core antigen;
KW pertussis toxin; tetanus toxin; measles virus F protein; immunotherapy;
KW Chlamydia trachomatis major outer membrane protein; immunogen; vaccine;
KW diphtheria toxin; plasmodium falciparum; circumsporozoite; E. coli TraT;
KW schistosoma mansoni; triose phosphate isomerase; allergenic reaction;
KW allergic rhinitis; food allergy; anaphylaxis; virally-induced asthma;
KW antihistamine; decongestant; beta-2 agonist; immunosuppression;
KW corticosteroid.
XX
OS Synthetic.
XX
PN WO9612740-A1.
XX
PD 02-MAY-1996.
XX
PF 25-OCT-1995; 95WO-US013841.
XX
PR 25-OCT-1994; 94US-00328519.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY, Walfield AM;
XX
DR WPI; 1996-230555/23.
XX
PT Peptide immunogen useful in treatment of allergy - comprises membrane-
PT bound IgE epsilon-chain peptide synthesised linearly in tandem with T
PT helper epitope peptide.
XX
PS Claim 2; Page 19; 53pp; English.
XX
CC AAW05957-W05616 represent helper T cell epitopes used in the peptide
CC immunogens of the invention. This sequence represents the tetanus toxin
CC helper T cell antigen. The peptides of the invention contain one of these
CC sequences, and a membrane-bound immunoglobulin E (IgE) fragment (see
CC AAW05595 and AAW05596). The peptide immunogens of the invention can be
CC used in vaccines for the immunotherapeutic treatment of allergenic
CC reactions, including allergic rhinitis, food allergies, anaphylaxis, or
CC virally-induced asthma. The immunogens overcome the short effective
CC period of antihistamines, decongestants, and beta-2 agonists, while
CC preventing the broad immunosuppression of corticosteroids. The peptides
CC do not have the potential side effects of restlessness or sedation
CC (associated with antihistamines), associated increased morbidity in
CC asthmatics (as seen with beta-2 agonists) and adverse hormonal activities
CC (observed in corticosteroid users)
XX
SQ Sequence 16 AA;

631-649

Query Match 56.6%; Score 56; DB 2; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.055;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 IIPYIGPALNI 13
              |:|||||||||
Db          5 IVPYIGPALNI 15
```

```
AAY96457
ID   AAY96457 standard; peptide; 20 AA.
XX
AC   AAY96457;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Tetanus toxin (TTD)-specific peptide residues 632-651.
XX
KW   Tetanus toxin; DTX; universal epitope; CD4-positive; immunodominant;
KW   antigen; infection; vaccine; immunostimulatory.
XX
OS   Synthetic.
XX
PN   WO200032626-A1.
XX
PD   08-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US028039.
XX
PR   25-NOV-1998;   98US-00199748.
XX
PA   (MINU ) UNIV MINNESOTA.
PA   (CONT/) CONTI-FINE B M.
XX
PI   Conti-Fine BM;
XX
DR   WPI; 2000-412286/35.
XX
PT   Isolated and purified peptide for immunization of mammal against
PT   infectious agent comprises amino acid sequence similar or identical to
PT   portion of amino acid sequence of antigen from infectious agent.
XX
PS   Example 4; Page 66; 108pp; English.
XX
CC   Peptides AAY96457-56 are tetanus toxoid (TTD) specific peptides capable
CC   of acting as universal epitopes. The peptides seem to be recognized by
CC   CD4 positive cells in humans, irrespective of their human leukocyte
CC   antigen (HLA) class II haplotype. These peptides and diphtheria toxin
CC   specific peptides (e.g. AAY96450-55) are useful as universal epitopes. A
CC   common structural feature of the peptides that may give them an advantage
CC   during processing is that they all include, or are flanked by, both at
CC   the N- and C-terminal ends, sequence regions forming relatively
CC   unstructured loops fully exposed to the solvent. Flanking exposed loops
CC   may be important for IRS formation as the loops would make easy targets
CC   for processing enzymes, resulting in the fast release of sequence
CC   segments embedded in the hydrophobic core of the antigenic molecule. The
CC   universal peptide epitopes can be used in vaccines against infectious
CC   agents (e.g. viruses, bacteria and fungi). The invention also provides
CC   methods of identifying immunogenic epitopes and IRS
XX
SQ   Sequence 20 AA;

  Query Match             56.6%;  Score 56;  DB 3;  Length 20;
  Best Local Similarity   90.9%;  Pred. No. 0.071;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:||||||||||
Db         10 IVPYIGPALNI 20
```

```
AAR82582
ID   AAR82582 standard; peptide; 16 AA.
XX
AC   AAR82582;
XX
DT   13-JUN-1996  (first entry)
XX
DE   Tetanus toxin helper T cell epitope, TT5.
XX
KW   IgE; CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope;
KW   vaccine; allergy; antibody; constant heavy chain.
XX
OS   Clostridium tetani.
XX
PN   WO9526365-A1.
XX
PD   05-OCT-1995.
XX
PF   24-MAR-1995;   95WO-US003741.
XX
PR   28-MAR-1994;   94US-00218461.
PR   25-OCT-1994;   94US-00328912.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 1995-351297/45.
XX
PT   Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper T
PT   cell epitope - useful for eliciting antibody prodn. for allergy
PT   treatment.
XX
PS   Claim 3; Page 23; 87pp; English.
XX
CC   AAR82571-91 are helper T cell epitopes which can be used in the
CC   preparation of a peptide immunogen that is useful in vaccines for
CC   treating allergic reactions. In the immunogen an IgE CH4 peptide is
CC   attached C-terminally to a series of amino acids including a helper T
CC   cell epitope. The immunogen may also opt. contain a fatty acid or fatty
CC   acid derivative, an invasin domain or alpha-NH2. The immunogen produces
CC   high titres of antibodies to the effector site in human IgE heavy chain
CC   (the CH4 domain peptide) which inhibit mast cell activation and reduce
CC   allergen-induced IgE prodn. The immunogens may be used in either a
CC   radially branching multimeric form or a linearly arranged monomeric form
XX
SQ   Sequence 16 AA;

  Query Match             52.5%;  Score 52;  DB 2;  Length 16;
  Best Local Similarity   90.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALN 12
              |:|||||||||
Db          5 IVPYIGPALN 14
```

AAR86583
ID AAR86583 standard; protein; 7 AA.
XX
AC AAR86583;
XX
DT 28-JUN-1996 (first entry)
XX
DE Autotaxin peptide fragment ATX-209.
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9532221-A2.
XX
PD 30-NOV-1995.
XX
PF 24-MAY-1995; 95WO-US006613.
XX
PR 25-MAY-1994; 94US-00249182.
PR 28-NOV-1994; 94US-00346455.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Stracke M, Liotta L, Schiffmann E, Krutzch J, Murata J;
XX
DR WPI; 1996-020533/02.
XX
PT Autotaxin motility stimulating protein, and DNA encoding it - used in
PT cancer diagnosis and therapy.
XX
PS Claim 4; Page 12; 112pp; English.
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is an
CC autocrine motility stimulating protein which is present in cancer cells.
CC ATX stimulates both random and directed migration of melanoma cells. The
CC tumourous form of ATX is a secreted protein, while the transmembrane
CC bound form is not present in tumour cells. The cDNA encoding this
CC sequence can be used in a vector, to transform cells. The recombinant
CC cells can then be used to produce the peptide sequences. Antibodies
CC specific for these sequences can be produced, and can be used in cancer
CC diagnosis and therapy. Different sites of localisation of the protein are
CC utilised for diagnosis and prognosis of the stages of tumour progression.
CC The sequences can be used in treatment methods to advantageously block
CC the activity of the secreted form of AXT, while having little effect on
CC the membrane form of AXT
XX
SQ Sequence 7 AA;

519-537

Query Match 31.9%; Score 30; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 LMPNIER 18
                :|||||:
Db          1 VMPNIEK 7
```

5204326-117
;Patent No. 5204326
;  APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
;  TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
;  NUMBER OF SEQUENCES: 147
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/493,359
;  FILING DATE: 14-MAR-1990
;SEQ ID NO:117:
;  LENGTH: 9
5204326-117

S19-537

Query Match 34.0%; Score 32; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLSSDIIG 8
              |||:|::|
Db          2 NLSTDVLG 9
```

```
Sequence 29, Application US/08447411
; Patent No. 5773243
;  GENERAL INFORMATION:
;    APPLICANT:  FRITZINGER, DAVID C.
;    APPLICANT:  BREDEHORST, REINHARD
;    APPLICANT:  VOGEL, CARL-WILHELM
;    TITLE OF INVENTION:  DNA ENCODING COBRA C3, CVF1, AND CVF2
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,411
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/043,747
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5773243man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-101-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-447-411-29

  Query Match             30.5%;  Score 32;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 KYELDK 15
              ||||||
Db          7 KYELDK 12
```

533-551

```
 Sequence 198, Application US/10658180
; Patent No. 6943002
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.DVUS02
;  CURRENT APPLICATION NUMBER: US/10/658,180
;  CURRENT FILING DATE:  2003-09-09
;  PRIOR APPLICATION NUMBER: US 09/755,630
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-10-658-180-198
```

547 ≥ 65

```
  Query Match             28.6%;  Score 30;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

```
RESULT 13
Q9R3Y4_CLOPE
ID   Q9R3Y4_CLOPE   PRELIMINARY;   PRT;    23 AA.
AC   Q9R3Y4;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Iota toxin component A (Fragment).
GN   Name=iap;
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=853, NCIB 10748, and 294;
RX   MEDLINE=98380411; PubMed=9712814;
RA   Billington S.J., Wieckowski E.U., Sarker M.R., Bueschel D.,
RA   Songer J.G., McClane B.A.;
RT   "Clostridium perfringens type E animal enteritis isolates with highly
RT   conserved, silent enterotoxin gene sequences.";
RL   Infect. Immun. 66:4531-4536(1998).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF037330; AAC34979.1; -; Genomic_DNA.
DR   EMBL; AF037328; AAC34977.1; -; Genomic_DNA.
DR   EMBL; AF037329; AAC34978.1; -; Genomic_DNA.
FT   NON_TER      23     23
SQ   SEQUENCE   23 AA;  2642 MW;  2DC67575E10BEC73 CRC64;

  Query Match             30.0%;  Score 30;  DB 2;  Length 23;
  Best Local Similarity   42.9%;  Pred. No. 3e+03;
  Matches    6;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 VKKVNKATEAAMFL 16
              :|||||:    : |
Db          1 MKKVNKSISVFLIL 14
```

Clm 93
589-607

```
Sequence 41, Application US/08346455B
; Patent No. 5731167
;  GENERAL INFORMATION:
;    APPLICANT:  UNITED STATES OF AMERICA; DEPT.
;    APPLICANT:  OF HEALTH AND HUMAN SERVICES
;    TITLE OF INVENTION:  MOTILITY STIMULATING
;    TITLE OF INVENTION:  PROTEIN USEFUL IN CANCER DIAGNOSIS AND
;    TITLE OF INVENTION:  THERAPY
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/346,455B
;      FILING DATE:  28-NOV-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06613
;      FILING DATE:  24-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/249,182
;      FILING DATE:  25-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/822,043
;      FILING DATE:  17-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOROTHY R. AUTH
;      REGISTRATION NUMBER:  36,434
;      REFERENCE/DOCKET NUMBER:  2026-4149PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7
;      TYPE:  amino acids
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Peptide
;    HYPOTHETICAL:  No
;    FEATURE:
;      NAME/KEY:  ATX-209
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-08-346-455B-41

  Query Match             31.9%;  Score 30;  DB 1;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 5e+05;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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519-537

```
Qy          12 LMPNIER 18
                :||||||:
Db           1 VMPNIEK 7
```

```
RESULT 1
US-11-347-179-294
; Sequence 294, Application US/11347179
; Publication No. US20060178503A1
; GENERAL INFORMATION:
;  APPLICANT: LUNDGREN-AKERLUND, EVY
;  TITLE OF INVENTION: INTEGRIN HETERODIMER AND A SUBUNIT THEREOF
;  FILE REFERENCE: 034341-001
;  CURRENT APPLICATION NUMBER: US/11/347,179
;  CURRENT FILING DATE:  2006-02-06
;  PRIOR APPLICATION NUMBER: US/09/647,544
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: PCT/SE99/00544
;  PRIOR FILING DATE: 1999-03-31
;  PRIOR APPLICATION NUMBER: SE 9900319.6
;  PRIOR FILING DATE: 1999-01-28
;  PRIOR APPLICATION NUMBER: SE 9801164-6
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 294
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-347-179-294

  Query Match             36.6%;  Score 34;  DB 7;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LNESINK 9
              |||||||
Db          8 LNESINK 14
```

qq 771-789

```
RESULT 47
C85939
hypothetical protein Z4183 [imported] - Escherichia coli (strain O157:H7, substrain ED
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85939
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85939
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27
A;Cross-references: UNIPROT:Q8X3L8; UNIPARC:UPI00000D0EF5; GB:AE005174; NID:g12517358;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4183

  Query Match             21.6%;  Score 22;  DB 2;  Length 27;
  Best Local Similarity   66.7%;  Pred. No. 5.7e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NKFLNQ 6
              :|||:|
Db          8 DKFLSQ 13
```

ca 785-803

```
RESULT 28
Q6EKS5_YERPE
ID   Q6EKS5_YERPE   PRELIMINARY;   PRT;    30 AA.
AC   Q6EKS5;
DT   16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT   16-AUG-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Hypothetical protein (Fragment).
OS   Yersinia pestis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Yersinia.
OX   NCBI_TaxID=632;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CIP 519/B2, CIP 548/B2, CIP 552/B3, CIP 557/B3, CIP 611/B4, CIP
RC   616/B4, CIP 685/B5, CIP CO92, and CIP 304;
RA   Roux V., Drancourt M., Raoult D.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY312300; AAQ94789.1; -; Genomic_DNA.
DR   EMBL; AY312301; AAQ94790.1; -; Genomic_DNA.
DR   EMBL; AY312302; AAQ94792.1; -; Genomic_DNA.
DR   EMBL; AY312303; AAQ94795.1; -; Genomic_DNA.
DR   EMBL; AY312304; AAQ94796.1; -; Genomic_DNA.
DR   EMBL; AY312305; AAQ94799.1; -; Genomic_DNA.
DR   EMBL; AY312306; AAQ94800.1; -; Genomic_DNA.
DR   EMBL; AY312307; AAQ94802.1; -; Genomic_DNA.
DR   EMBL; AY312299; AAQ94786.1; -; Genomic_DNA.
DR   InterPro; IPR007473; DUF519.
DR   Pfam; PF04378; DUF519; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   30 AA;  3417 MW;  F46332581AF6AC90 CRC64;

  Query Match             27.5%;  Score 28;  DB 2;  Length 30;
  Best Local Similarity   57.1%;  Pred. No. 7.1e+03;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 MNSMIPY 19
                 |||::|:
Db          3 MNSLLPW 9
```

785-803

```
RESULT 28
US-10-946-371-33
; Sequence 33, Application US/10946371
; Publication No. US20050208587A1
; GENERAL INFORMATION:
;  APPLICANT: CARDOSO, ROSA
;  APPLICANT:  WILSON, IAN
;  APPLICANT:  BURTON, DENNIS
;  APPLICANT:  DAWSON, PHILIP
;  TITLE OF INVENTION: PEPTIDES THAT BIND TO BROADLY NEUTRALIZING ANTI-HIV
;  TITLE OF INVENTION:  ANTIBODY-STRUCTURE OF 4E10 FAB FRAGMENT COMPLEX, USES
;  TITLE OF INVENTION:  THEREOF, COMPOSITIONS THEREFROM
;  FILE REFERENCE: 678501-2001.1
;  CURRENT APPLICATION NUMBER: US/10/946,371
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: 60/504,123
;  PRIOR FILING DATE: 2003-09-19
;  PRIOR APPLICATION NUMBER: PCT/EP02/10070
;  PRIOR FILING DATE: 2002-09-09
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 33
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-946-371-33

  Query Match             35.7%;  Score 35;  DB 5;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          9 TNWLAK 14
```

715-733

```
  d s
Set     Items   Description
S1       6814   S E2-E4
S2         71   S E2-E17
S3        916   S E41-E46
S4        175   'BOTULINUM TOXIN BTX':'BOTULINUM TOXIN C 2' OR E44-E48 FROM 155, 5, 34,
35, 45, 65, 71, 73, 91, 94, 98, 135, 144, 149, 156, 159, 162, 164, 172, 266, 369, 370,
399, 434, 444, 467
S5       7196   S S1 OR S2 OR S3 OR S4
S6     221938   'EPITOPE' FROM 155, 5, 34, 35, 45, 65, 71, 73, 91, 94, 98, 135, 144, 149,
156, 159, 162, 164, 172, 266, 369, 370, 399, 434, 444, 467
S7       4234   'MAPPING //EPITOPE'  (EPITOPE MAPPING) FROM 155, 5, 34, 35, 45, 65, 71,
73, 91, 94, 98, 135, 144, 149, 156, 159, 162, 164, 172, 266, 369, 370, 399, 434, 444, 467
È
S8         21   S S5 AND (S6 OR S7)
S9         20   RD  (unique items)

?  t s9/9/9 10 11 12 13-20
```

9/9/9 (Item 7 from file: 73) **Links**

EMBASE



11955596 **EMBASE No:** 2003066469

**Overview of the needs and realities for developing new and improved vaccines in the 21st century**

Hilleman M.R.

Dr. M.R. Hilleman, Merck Institute for Vaccinology, Merck and Co., Inc. (WP53C-350), 770 Sumneytown Pike, West Point, PA 19486 United States

**Author Email:** maurice hilleman@merck.com

Intervirology ( INTERVIROLOGY ) ( Switzerland ) 2002 , 45/4-6 (199-211)

**CODEN:** IVRYA **ISSN:** 0300-5526

**Document Type:** Journal ; Conference Paper

**Language:** ENGLISH **Summary Language:** ENGLISH

**Number Of References:** 90

The science of present day vaccinology is based on the pioneering discoveries of the late 18th and late 19th centuries and the technologic breakthroughs of the past 60 years. The driving force for the development of new vaccines resides in technologic feasibility, public need and economic incentive for translating the basic knowledge into a product. Past efforts by government to define which particular vaccines to develop were mostly irrelevant to the realistic choices which were made. There is a vast array of viral, bacterial, parasitic and fungal disease agents against which preventative vaccines may be developed, and to this may be added cancer and certain amyloidoses such as Alzheimer's and 'mad cow' diseases. The proven past for vaccines has relied on live, killed, protein and polysaccharide antigens plus the single example of recombinant-expressed hepatitis B vaccine. The validity of redirection of vaccinology to exploration of simplified vaccines such as recombinant vectored and DNA preparations and reductionist vaccines based on peptides of contrived **epitope** composition remains to be proved. Reductionism imposes vastly increased complexity and difficulty on vaccine development and might not be capable of achievement. The challenge in the 21st century will involve new and uncertain pathways toward worthwhile accomplishments. Copyright (c) 2003 S. Karger AG, Basel.

**DRUG DESCRIPTORS:**

* bacterial vaccine--drug development--dv; *virus vaccine--drug development --dv

hepatitis B vaccine; polysaccharide; antigen; DNA vaccine; diphtheria vaccine; tetanus toxoid; pertussis v

**botulinum toxin A**; Lyme disease vaccine; Pneumococcus vaccine; Meningococcus vaccine; influenza vaccine; BCG vaccine; typhoid vaccine; cholera vaccine; anthrax vaccine; poliomyelitis vaccine; measles vaccine; mumps vaccine; rubella vaccine; chickenpox vaccine; yellow fever vaccine; hepatitis A vaccine; rabies vaccine; Rotavirus vaccine; respiratory syncytial virus vaccine; parainfluenza vaccine; unindexed drug

**MEDICAL DESCRIPTORS:**

* vaccination; *bacterial infection--etiology--et; *bacterial infection --prevention--pc; *virus infection--etiology--et; *virus infection --prevention--pc

immune response; drug targeting; cancer immunization; amyloidosis; responsibility; government; Alzheimer disease; bovine spongiform encephalopathy; human; nonhuman; conference paper; priority journal

**CAS Registry Number:** 57425-69-1, 93384-51-1 (tetanus toxoid); 93384-43-1 (**botulinum toxin A**)

**Section Headings:**

004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
008 Neurology and Neurosurgery
016 Cancer
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/10 (Item 8 from file: 73) **Links**
EMBASE

11542312 **EMBASE No:** 2002114797

**Characterisation of monoclonal antibodies against haemagglutinin associated with Clostridium botulinum type C neurotoxin**

Mahmut N.; Inoue K.; Fujinaga Y.; Hughes L.; Arimitsu H.; Sakaguchi Y.; Ohtsuka A.; Murakami T.; Yokota K.; Oguma K.
Dr. K. Oguma, Department of Bacteriology, Okayama Univ. Grad. Sch. Med./Dent., 2-5-1 Shikata-cho, Okayama 700-8558 Japan
**Author Email:** kuma@md.okayama-u.ac.jp
Journal of Medical Microbiology ( J. MED. MICROBIOL. ) ( United Kingdom ) 2002 , 51/4 (286-294)
**CODEN:** JMMIA **ISSN:** 0022-2615
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 12

Of 11 monoclonal antibodies (MAbs) prepared against the non-toxic component of type C Clostridium botulinum 16S toxin to clarify the function of the non-toxic component, seven recognised HA1, three recognised HA3b and one recognised HA2. Results of **epitope** mapping indicated that three of the seven anti-HA1 MAbs recognised the region between amino acid residues 121 and 140 and four recognised the three-dimensional structure of HA1. Three anti-HA3b MAbs recognised different regions between (approximately) amino acids 405-430, 180-270 and 275-297. The ability of these MAbs to interfere with binding of 16S toxin or non-toxic component, HA1 or HA3b to erythrocytes and to intestine tissue sections of guinea-pig was observed. MAbs against HA3b and HA2 did not inhibit 16S toxin binding to either erythrocytes or epithelial cells, whereas some MAbs against HA1 did inhibit binding. The seven anti-HA1 MAbs can be classified into four groups based on their binding inhibition activities. The anti-HA1 MAbs that inhibited the binding of 16S toxin to the epithelial cells also neutralised or reduced the oral toxicity in mice, indicating that HA may play an important role in the absorption of the 16S toxin from the small intestine.

**DRUG DESCRIPTORS:**
* monoclonal antibody; *hemagglutinin--endogenous compound--ec; *neurotoxin --drug toxicity--to; *neurotoxin--endogenous compound--ec; *botulinum toxin --drug toxicity--to; *botulinum toxin--endogenous compound--ec
amino acid--endogenous compound--ec; neutralizing antibody; unclassified drug
**MEDICAL DESCRIPTORS:**
* Clostridium botulinum; *protein function
**epitope** mapping; antibody structure; antigen binding; inhibition kinetics; binding site; molecular recognition; erythrocyte; epithelium cell ; intestine epithelium; guinea pig; toxin analysis; intestine absorption; nonhuman; female; mouse; animal experiment; animal tissue; animal cell; article; priority journal
**Drug Terms (Uncontrolled): botulinum toxin c**--drug toxicity--to; **botulinum toxin c** --endogenous compound--ec
**CAS Registry Number:** 37333-12-3 (hemagglutinin); 39386-17-9 (neurotoxin); 65072-01-7 (amino acid )
**Section Headings:**
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
026 Immunology, Serology and Transplantation

9/9/11 (Item 9 from file: 73) **Links**
EMBASE

11505346 **EMBASE No:** 2002076810

**Genetic and immunological comparison of anti-botulinum type A antibodies from immune and non-immune human phage libraries**

Amersdorfer P.; Wong C.; Smith T.; Chen S.; Deshpande S.; Sheridan R.; Marks J.D.
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**Author Email:** peter amersdorfer@corvas.com
Vaccine ( VACCINE ) ( United Kingdom ) 22 FEB 2002 , 20/11-12 (1640-1648)
**CODEN:** VACCD **ISSN:** 0264-410X
**Publisher Item Identifier:** S0264410X01004820
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 44

Understanding the antibody response in botulinum intoxication is important for vaccine design and passive prophylaxis. To investigate this activity, we have studied the immune response to BoNT/A (botulinum neurotoxin serotype A) binding domain (HSUBC) at the molecular level using phage display. The scFv antibodies were isolated from V-gene repertoires prepared from (a) human volunteer immunized with pentavalent botulinum toxoid and (b) non-immune human peripheral blood lymphocytes and spleenocytes. A large panel of serotype specific phage expressing botulinum binding scFv could be selected from both libraries. **Epitope** mapping of immune scFv binders towards BoNT/A HSUBC revealed surprisingly a limited number of scFv recognizing conformational epitopes that corresponded to two distinct groups, clusters I and II. Only scFv from cluster I exhibited neutralizing activity in the mouse hemidiaphragm assay. Anti- BoNT/A HSUBC clones derived from a non-immune library could be conveniently grouped into clusters III-XI and appeared to share no overlapping epitopes with cluster I or II. In addition they showed no neutralization of toxin at biologically significant concentrations. We therefore suggest that a vaccine based on the pentavalent botulinum toxoid directs the humoral immune response to a limited number of immunodominant epitopes exposed on the binding domain HSUBC. (c) 2002 Elsevier Science Ltd. All rights reserved.

**DRUG DESCRIPTORS:**
* **botulinum toxin A**--pharmacology--pd; ***epitope**--pharmacology --pd; *single chain fragment variable antibody--drug comparison--cm; * single chain fragment variable antibody--pharmacology--pd; *neutralizing antibody--drug comparison--cm; *neutralizing antibody--pharmacology--pd; * vaccine--drug comparison--cm; *vaccine--pharmacology--pd
botulinum toxin--pharmacology--pd; unclassified drug
**MEDICAL DESCRIPTORS:**
* botulism--etiology--et; *antibody library
phage display; immune response; antibody isolation; immunization; binding site; lymphocyte; spleen cell; serotype; bacteriophage; protein expression; **epitope** mapping; antigen binding; antigen recognition; antibody combining site; drug activity; hemidiaphragm; vaccine production; humoral immunity; nonhuman; male; mouse; animal model; controlled study; animal tissue; article; priority journal
**Drug Terms (Uncontrolled):** botulinum toxin a antibody--drug comparison--cm; botulinum toxin a antibody --pharmacology--pd

**CAS Registry Number:** 93384-43-1 (**botulinum toxin A**); 334577-34-3, 334577-38-7 (single chain fragment variable antibody)

**Section Headings:**

004 Microbiology: Bacteriology, Mycology, Parasitology and Virology

026 Immunology, Serology and Transplantation

037 Drug Literature Index

9/9/12 (Item 10 from file: 73) **Links**
EMBASE

11319442 **EMBASE No:** 2001333655
**Epitope mapping of neutralizing botulinum neurotoxin A antibodies by phage display**

Mullaney B.P.; Pallavicini M.G.; Marks J.D.
B.P. Mullaney, UCSF Cancer Center, Box 0808, UCSF, San Francisco, CA 94143-0808 United States
**Author Email:** mullaney@cc.ucsf.edu
Infection and Immunity ( INFECT. IMMUN. ) ( United States ) 2001 , 69/10 (6511-6514)
**CODEN:** INFIB **ISSN:** 0019-9567
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 27

Single-chain antibodies neutralize activity and bind nonoverlapping epitopes of botulinum A neurotoxin. Two phage display **epitope** libraries were constructed from the 1.3 kb of binding domain cDNA. The minimal epitopes selected against the single-chain Fv-Fc antibodies correspond to conformational epitopes with amino acid residues 1115 to 1223 (S25), 1131 to 1264 (3D12), and 889 to 1294 (C25).

**Molecular Sequence Number:** ; GENBANK, U22962
**DRUG DESCRIPTORS:**
*** epitope**; ***botulinum toxin A**; *neutralizing antibody; *Fc receptor
**MEDICAL DESCRIPTORS:**
* gene mapping; *Clostridium botulinum; *nucleotide sequence
bacteriophage; antigen binding; DNA library; protein domain; amino acid sequence; protein conformation; drug receptor binding; gel electrophoresis; DNA sequence; molecular model; crystal structure; article; priority journal
**CAS Registry Number:** 93384-43-1 **(botulinum toxin A)**
**Section Headings:**
026 Immunology, Serology and Transplantation
029 Clinical and Experimental Biochemistry

9/9/13 (Item 11 from file: 73) **Links**
EMBASE

10973449 **EMBASE No:** 2001017400

**Light chain of botulinum a neurotoxin expressed as an inclusion body from a synthetic gene is catalytically and functionally active**

Ahmed S.A.; Smith L.A.
L.A. Smith, Dept. of Immunol. and Molec. Biology, Toxinology Division, U.S. Army Medical Research Institute, 1425 Porter Street, Fort Detrick, MD 21702 United States
**Author Email:** leonard.smith@amedd.army.mil
Journal of Protein Chemistry ( J. PROTEIN CHEM. ) ( United States ) 2000 , 19/6 (475-487)
**CODEN:** JPCHD **ISSN:** 0277-8033
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 46

Botulinum neurotoxins, the most potent of all toxins, induce lethal neuromuscular paralysis by inhibiting exocytosis at the neuromuscular junction. The light chains (LC) of these dichain neurotoxins are a new class of zinc-endopeptidases that specifically cleave the synaptosomal proteins, SNAP-25, VAMP, or syntaxin at discrete sites. To facilitate the structural and functional characterization of these unique endopeptidases, we constructed a synthetic gene for the LC of the botulinum neurotoxin serotype A (BoNT/A), overexpressed it in Escherichia coli, and purified the gene product from inclusion bodies. Our procedure can provide 1.1 g of the LC from 1 L of culture. The LC product was stable in solution at 4degreesC for at least 6 months. This rBoNT/A LC was proteolytically active, specifically cleaving the Glu-Arg bond in a 17-residue synthetic peptide of SNAP-25, the reported cleavage site of BoNT/A. Its calculated catalytic efficiency kSUBcat/KSUBm was higher than that reported for the native BoNT/A dichain. Treating the rBoNT/A LC with mercuric compounds completely abolished its activity, most probably by modifying the cysteine-164 residue located in the vicinity of the active site. About 70% activity of the LC was restored by adding ZnSUP2+ to a ZnSUP2+ - free, apo-LC preparation. The LC was nontoxic to mice and failed to elicit neutralizing **epitope**(s) when the animals were vaccinated with this protein. In addition, injecting rBoNT/A LC into sea urchin eggs inhibited exocytosis-dependent plasma membrane resealing. For the first time, results of our study make available a large amount of the biologically active toxin fragment in a soluble and stable form.

**DRUG DESCRIPTORS:**
* **botulinum toxin A**--drug toxicity--to
neurotoxin--drug toxicity--to
**MEDICAL DESCRIPTORS:**
* neurotoxicity--etiology--et; *cell inclusion; *neuromuscular synapse paralysis--etiology--et; toxin analysis; exocytosis; peptide analysis; Escherichia coli; gene expression; vaccination; nonhuman; male; mouse; animal experiment; article
**CAS Registry Number:** 93384-43-1 (**botulinum toxin A**); 39386-17-9 (neurotoxin)
**Section Headings:**
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
008 Neurology and Neurosurgery
026 Immunology, Serology and Transplantation
052 Toxicology

9/9/14 (Item 12 from file: 73) **Links**
EMBASE

10971923 **EMBASE No:** 2001015519
**High-affinity, protective antibodies to the binding domain of botulinum neurotoxin type A**

Pless D.D.; Torres E.R.; Reinke E.K.; Bavari S.
S. Bavari, Dept. of Cell Biology/Biochemistry, U.S. Army Med. Res. Inst. Inf. Dis., 1425 Porter St., Frederick, MD 21702-5011 United States
**Author Email:** Sina.Bavari@AMEDD.Army.Mil
Infection and Immunity ( INFECT. IMMUN. ) ( United States ) 2001 , 69/1 (570-574)
**CODEN:** INFIB **ISSN:** 0019-9567
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 19

Monocionai antibodies (MAbs) were prepared against the putative binding domain of botulinum neurotoxin A (BoNT/A), a nontoxic 50-kDa fragment. Initially, all fusion products were screened against the holotoxin BoNT/A and against the binding fragment, BoNT/A HSUBC. Eleven neutralizing hybridomas were cloned, and their specific binding to BoNT/A HSUBC was demonstrated by surface plasmon resonance, with dissociation constants ranging from 0.9 to <0.06 nM. **Epitope** mapping by real-time surface plasmon resonance showed that the antibodies bound to at least two distinct regions of the BoNT/A HSUBC fragment. These MAbs will be useful tools for studying BoNT/A interactions with its receptor, and they have potential diagnostic and therapeutic applications.

**DRUG DESCRIPTORS:**
*** botulinum toxin A**; *monoclonal antibody--intraperitoneal drug administration--ip
**MEDICAL DESCRIPTORS:**
* antibody production; *antigen binding
binding site; hybridoma; **epitope** mapping; dissociation constant; molecular interaction; kinetics; nonhuman; mouse; animal experiment; controlled study; animal cell; article; priority journal
**CAS Registry Number:** 93384-43-1 **(botulinum toxin A)**
**Section Headings:**
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/15 (Item 13 from file: 73) **Links**
EMBASE

10894888 **EMBASE No:** 2000379437

**Anomalous enhancement of botulinum toxin type A neurotoxicity in the presence of antitoxin**

Sheridan R.E.; Deshpande S.S.; Amersdorfer P.; Marks J.D.; Smith T.
R.E. Sheridan, Neurotoxicology Branch, Pharmacology Division, US Army Medical Research Institute, 3100 Ricketts Point Road, Aberdeen Proving Ground, MD 21010 United States
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Toxicon ( TOXICON ) ( United Kingdom ) 2001 , 39/5 (651-657)
**CODEN:** TOXIA **ISSN:** 0041-0101
**Publisher Item Identifier:** S0041010100001896
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 13

The neutralization of botulinum toxin serotype A with polyclonal equine antitoxin was studied in isolated mouse hemidiaphragms and compared to the same action in live mice. The biological activity of the toxin in the isolated muscle could be markedly reduced with excess antitoxin, estimated as 3:1 molar ratios of IgG Ab:toxin or better. Toxin neutralization in vivo required higher ratios of Ab:toxin, ranging from 30:1 at high toxin doses and increasing to 100:1 at 10xLD50 toxin. At equimolar Ab to toxin ratios in the isolated muscle, the biological activity of the toxin underwent a statistically significant increase. This paradoxical effect of the polyclonal antisera was serotype selective and independent of the presence or absence of hemagglutinin in the toxin. The enhancement of toxin activity was subsequently localized to occupancy of one of four epitopes on the toxin using monoclonal antibodies to mimic the effect of the antitoxin. The enhancement of toxin activity suggests that botulinum toxin may undergo a conformational change upon binding antibodies to certain domains. This phenomenon could contribute to the observed concentration dependent changes in neutralization efficacy with antitoxin in vivo. Copyright (C) 2000 .

**DRUG DESCRIPTORS:**
* **botulinum toxin A**--drug toxicity--to; *antitoxin--pharmacology--pd; *neurotoxin--drug toxicity--to **epitope**; hemagglutinin--endogenous compound--ec; cell surface receptor--endogenous compound--ec; monoclonal antibody--pharmacology--pd

**MEDICAL DESCRIPTORS:**
* neurotoxicity--etiology--et; *botulism--etiology--et; *toxicity testing
drug activity; nonhuman; male; mouse; animal experiment; animal model; controlled study; animal tissue; article; priority journal

**CAS Registry Number:** 93384-43-1 (**botulinum toxin A**); 39386-17-9 (neurotoxin); 37333-12-3 (hemagglutinin)
**Section Headings:**
037 Drug Literature Index
052 Toxicology
008 Neurology and Neurosurgery

infection--epidemiology--ep; human; nonhuman; conference paper; priority journal
**CAS Registry Number:** 93384-43-1 (**botulinum toxin A**); 39386-17-9 (neurotoxin)
**Section Headings:**
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
008 Neurology and Neurosurgery
037 Drug Literature Index
052 Toxicology

9/9/17 (Item 15 from file: 73) **Links**
EMBASE

07757198 **EMBASE No:** 1999241087

**Structure, activity, and immune (T and B cell) recognition of botulinum neurotoxins**

Atassi M.Z.; Oshima M.
M.Z. Atassi, Department of Biochemistry, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030 United States
Critical Reviews in Immunology ( CRIT. REV. IMMUNOL. ) ( United States ) 1999 , 19/3 (219-260)
**CODEN:** CCRID **ISSN:** 1040-8401
**Document Type:** Journal ; Review
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 271

Botulism, which was first reported over a century ago, is caused by botulinum neurotoxins produced by Clostridium botulinum in seven immunological serotypes (A through G). The primary structures of a number of these BoNTs have been determined and are reviewed here, together with their gene structure and synthesis. The biological actions of BoNTs, which result in their ability to block neurotransmitter release have been the subject of intensive study, and in this review we discuss the binding of BoNTs to the cell surface as well as the mechanism of their intercellular action. The ability of BoNTs to block neurotransmitter release has been exploited in therapeutic applications to reduce muscle hyperactivity for the treatment of a variety of clinical conditions associated with involuntary muscle spasm and contractions. The advantages, limitations, and risks of these applications are discussed. Certain compounds provide some limited protection against BoNT. However, more effective protection has been obtained immunologically either by passive immunity (i.e., by administration of anti-BoNT Abs) or by immunization with inactivated toxin. More recently, excellent protection has been obtained by immunization with the receptor-binding region comprising the C-terminal (residues 860 to 1296) fragment (H(C)) of the heavy chain of BoNT/A. Here we review the mapping of the epitopes on the Hc region of BoNT/A that are recognized by anti-BoNT/A Abs raised in horse, human, and mouse. The epitopes on the H(C) that are recognized by anti-H(C) Abs and by H(C)-primed T lymphocytes were mapped in two mouse strains [BALB/c (H-2(d)) and SJL (H- 2(s))]. The peptides, which contain Ab or T cell epitopes (or both) on the H(C), were used as immunogens in BALB/c and SJL mice and we identified those peptides whose Ab and/or T-cell responses cross-react with H(C). Identification of these peptides is an important first step in the intricate requirements for the design of a synthetic vaccine.

**DRUG DESCRIPTORS:**
*** botulinum toxin a**; *neurotransmitter--endogenous compound--ec; * inactivated vaccine--drug therapy--dt; ***epitope**--endogenous compound --ec
**MEDICAL DESCRIPTORS:**
* antigen recognition; *t lymphocyte; *b lymphocyte
botulism--drug therapy--dt; botulism--prevention--pc; gene structure; neurotransmitter release; passive immunization; carboxy terminal sequence; cross reaction; human; nonhuman; mouse; review; priority journal
**CAS Registry Number:** 93384-43-1 (**botulinum toxin a**)
**Section Headings:**
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/18 (Item 16 from file: 73) **Links**
EMBASE

07203386 **EMBASE No:** 1998096328

**Antibodies and T cells against synthetic peptides of the C-terminal domain (H(c)) of botulinum neurotoxin type A and their cross-reaction with H(c)**

Oshima M.; Middlebrook J.L.; Atassi M.Z.
M.Z. Atassi, Department of Biochemistry, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030 United States
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Immunology Letters ( IMMUNOL. LETT. ) ( Netherlands ) 1998 , 60/1 (7-12)
**CODEN:** IMLED **ISSN:** 0165-2478
**Publisher Item Identifier:** S0165247897001247
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 21

Seventeen peptides containing T cell and/or antibody (Ab) epitopes previously localized on H(c) of botulinum neurotoxin type A were used in SJL and BALB/c mice as immunogens either individually or as an equimolar mixture of groups that contained epitopes of T cells, Abs or both, to determine their abilities to generate T cells and/or Abs that recognize intact H(c). In SJL, peptide 897-915 which included both T cell and Ab epitopes, elicited Abs that cross-reacted very strongly with H(c). In BALB/c, peptides 869-887, 883-901, 981-999 and 1275-1296 which contained Ab epitopes generated Abs that cross- reacted strongly with H(c). A mixture of peptides that contained T cell and Ab epitopes was effective in both strains in eliciting T cells and Abs that cross-reacted with H(c). This mixture form gave a quicker rise (after two injections) in cross-reactive (with H(c)) Ab titer as compared to other peptide mixtures or the individual peptides, and sustained in BALB/c a high Ab titer upon further booster injections. Some of the regions that elicited crossreactive immunity to H(c) have sequence similarity to other clostridial toxins, suggesting that one or more of these synthetic peptides might provide cross-protection against those toxins.

**DRUG DESCRIPTORS:**
* **botulinum toxin a**; *synthetic peptide--drug development--dv; * bacterial vaccine--drug development--dv neurotoxin; **epitope**; cross reacting antibody
**MEDICAL DESCRIPTORS:**
* botulism--etiology--et; *botulism--prevention--pc; *t lymphocyte; * immunization neurotoxicity--etiology--et; neurotoxicity--prevention--pc; lymph node cell ; lymphocyte proliferation; peptide synthesis; cross reaction; antibody titer; clostridium botulinum; nonhuman; mouse; animal model; animal cell; subcutaneous drug administration; article; priority journal
**CAS Registry Number:** 93384-43-1 (**botulinum toxin a**); 39386-17-9 (neurotoxin)
**Section Headings:**
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/19 (Item 17 from file: 73) **Links**
EMBASE

07000286 **EMBASE No:** 1997286617

**Molecular characterization of murine humoral immune response to botulinum neurotoxin type A binding domain as assessed by using phage antibody libraries**

Amersdorfer P.; Wong C.; Chen S.; Smith T.; Deshpande S.; Sheridan R.; Finnern R.; Marks J.D.
J.D. Marks, University of California, San Francisco General Hospital, 1001 Potrero Ave., San Francisco, CA 94110 United States
Infection and Immunity ( INFECT. IMMUN. ) ( United States ) 1997 , 65/9 (3743-3752)
**CODEN:** INFIB **ISSN:** 0019-9567
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 51

To produce antibodies capable of neutralizing botulinum neurotoxin type A (BoNT/A), the murine humoral immune response to BoNT/A binding domain (H(C)) was characterized at the molecular level by using phage antibody libraries. Mice were immunized with BoNT/A H(C), the spleens were harvested, and single-chain Fv (scFv) phage antibody libraries were constructed from the immunoglobulin heavy and light chain variable region genes. Phage expressing BoNT/A binding scFv were isolated by selection on immobilized BoNT/A and BoNT/A H(C). Twenty-eight unique BoNT/A H(C) binding scFv were identified by enzyme-linked immunosorbent assay and DNA sequencing. **Epitope** mapping using surface plasmon resonance in a BIAcore revealed that the 28 scFv bound to only 4 nonoverlapping epitopes with equilibrium constants (K(d)) ranging from 7.3 x 10sup - sup 8 to 1.1 x 10sup -sup 9 M. In a mouse hemidiaphragm assay, scFv binding epitopes 1 and 2 significantly prolonged the time to neuroparalysis, 1.5- and 2.7-fold, respectively, compared to toxin control. scFv binding to epitopes 3 and 4 showed no protection against neuroparalysis. A combination of scFv binding epitopes 1 and 2 had an additive effect on time to neuroparalysis, which increased to 3.9-fold compared to the control. The results suggest that there are two 'productive' receptor binding sites on H(C) which lead to toxin internalization and toxicity. Blockade of these two epitopes with monoclonal antibodies may provide effective immunoprophylaxis or therapy against BoNT/A intoxication.

**DRUG DESCRIPTORS:**
*** botulinum toxin a**
**MEDICAL DESCRIPTORS:**
* binding site; *humoral immunity
antibody production; article; bacteriophage; dna library; immunization; immunoprophylaxis; internalization; molecular genetics; nonhuman; phage display; priority journal
**CAS Registry Number:** 93384-43-1 **(botulinum toxin a)**
**Section Headings:**
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology

9/9/20 (Item 18 from file: 73) Links
EMBASE

06853948 **EMBASE No:** 1997136549

**Antibody mapping to domains of botulinum neurotoxin serotype A in the complexed and uncomplexed forms**

Chen F.; Kuziemko G.M.; Amersdorfer P.; Wong C.; Marks J.D.; Stevens R.C.
J.D. Marks, Anesthesia/Pharmaceut. Chem. Dept., University of California, SFGH, 1001 Potrero, San Francisco, CA 94110 United States
Infection and Immunity ( INFECT. IMMUN. ) ( United States ) 1997 , 65/5 (1626-1630)
**CODEN:** INFIB **ISSN:** 0019-9567
**Document Type:** Journal ; Article
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 28

The domain organization of the botulinum neurotoxin serotype A was studied by using antibody mapping of 44 monoclonal single-chain variable fragments. The analysis was carried out on (i) the individual domains of botulinum neurotoxin holotoxin (binding, translocation, and catalytic), (ii) botulinum neurotoxin holotoxin, (iii) the botulinum neurotoxin holotoxin in complex with the nontoxic portion, and (iv) botulinum neurotoxin holotoxin and nontoxic portion of the complex recombined in vitro. All 44 antibodies mapped to individual domains of botulinum neurotoxin. Forty of the 44 single-chain variable fragments bound the botulinum neurotoxin holotoxin relative to the isolated domains, suggesting that 4 epitopes are covered when the individual domains are in the holotoxin form. Only 20 of the antibodies showed a positive reaction to the toxin while in complex with the nontoxic portion. All of the covered epitopes were mapped to the binding domain of botulinum neurotoxin, which suggested that the binding domain is in direct contact with the nontoxic portion in the complex. Based on the antibody mapping to the different domains of the botulinum neurotoxin holotoxin and the entire complex, a model of the botulinum neurotoxin complex is proposed.

**DRUG DESCRIPTORS:**
* **botulinum toxin a**--endogenous compound--ec
**epitope**
**MEDICAL DESCRIPTORS:**
* botulism--etiology--et; *clostridium botulinum
antigen antibody complex; antigen recognition; article; nonhuman; priority journal; serotype; toxin analysis
**CAS Registry Number:** 93384-43-1 (**botulinum toxin a**)
**Section Headings:**
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
026 Immunology, Serology and Transplantation

9/9/16 (Item 14 from file: 73) **Links**
EMBASE

10594483 **EMBASE No:** 2000060235

# Botulism: Laboratory methods and epidemiology

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**Author Email:** rfernand@fmed2.uncu.edu.ar
Anaerobe ( ANAEROBE ) ( United Kingdom ) 1999 , 5/3-4 (165-168)
**CODEN:** ANAEF **ISSN:** 1075-9964
**Document Type:** Journal ; Conference Paper
**Language:** ENGLISH **Summary Language:** ENGLISH
**Number Of References:** 27

Although food botulism (FB) in Argentina was described by 1911, the first documented outbreak was recorded in 1922. In 1957, an outbreak of type A FB caused by red bell peppers was the first laboratory confirmation of botulism in Argentina. From 1922 to 1997, 70 FB outbreaks affecting 242 persons with 111 deaths (case fatality rate, 46%) were reported in Argentina. Infant botulism (IB) was recognized in 1976 and has been mostly diagnosed in the U.S.A. More than 146 IB cases have been reported in Argentina since 1982. Additional cases may go undiagnosed due to physician inexperience and limited access to diagnostic services. A single laboratory-confirmed case of wound botulism (WB) occurred in Argentina in 1995. The botulinal neurotoxins (BoNTs) identified in Argentina have been types A, B, E, F and Af in FB, and exclusively type A in IB and WB. For the laboratory diagnosis of botulism, serum, gastrointestinal sample, food, and wounds should be tested for BoNT. Gastrointestinal, wound and food sample must also be cultured for toxigenic organisms. When higher volumes of serum were tested, BoNT was found in 61% of IB patients in Mendoza compared with 13% in a previous series from the U.S.A. Reliable typing can only be achieved when the BoNT belongs to a known serotype and the toxin titer is above 4000 LDinf 5inf 0/mL. When these criteria are not met, as in most clinical samples, bacterial isolation, purification and adequate toxin production in culture are required. Neutralization testing must be performed at not less than three 10-fold doses of toxin because of (1) the existence of subtypes, where a second, minor serotype is present, (2) the sharing of epitopes between certain serotypes, and (3) the occurrence of serological variants. Three basic properties of working antitoxins, specificity, protency and avidity, must be known for BoNT typing. The efficiency index (EI), which expresses the avidity of antitoxins, is an important instrument for recognizing BoNT subtypes. (C) 1999 Academic Press.

**DRUG DESCRIPTORS:**
antibiotic agent--drug therapy--dt; antitoxin--drug therapy--dt; **botulinum toxin A**--endogenous compound--ec; **botulinum toxin B** --endogenous compound--ec; **epitope**--endogenous compound--ec; neurotoxin--endogenous compound--ec

**MEDICAL DESCRIPTORS:**
* botulism--complication--co; *botulism--diagnosis--di; *botulism--drug therapy--dt; *botulism--epidemiology--ep Argentina; Clostridium botulinum; LD 50; United States; bacterium isolation ; food analysis; food poisoning--diagnosis--di; food poisoning--drug therapy--dt; food poisoning--epidemiology--ep; gastrointestinal tract; infant disease--diagnosis--di; infant disease--drug therapy--dt; infant disease--epidemiology--ep; laboratory diagnosis; mortality; pepper; purification; sampling; serotype; titrimetry; toxin synthesis; wound infection--complication--co; wound infection--diagnosis--di; wound infection--drug therapy--dt; wound

052 Toxicology

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 615 | 22 | 23.4 | 25 | 2 | Q56C76_9HIV1 | Q56c76 | human immun |
| 616 | 22 | 23.4 | 25 | 2 | Q56C77_9HIV1 | Q56c77 | human immun |
| 617 | 22 | 23.4 | 25 | 2 | Q56C78_9HIV1 | Q56c78 | human immun |
| 618 | 22 | 23.4 | 25 | 2 | Q56C79_9HIV1 | Q56c79 | human immun |
| 619 | 22 | 23.4 | 25 | 2 | Q71940_9HIV1 | Q71940 | human immun |
| 620 | 22 | 23.4 | 25 | 2 | Q71946_9HIV1 | Q71946 | human immun |
| 621 | 22 | 23.4 | 25 | 2 | Q8QE38_9HIV1 | Q8qe38 | human immun |
| 622 | 22 | 23.4 | 25 | 2 | Q9IQQ5_9HIV1 | Q9iqq5 | human immun |
| 623 | 22 | 23.4 | 26 | 1 | MEL_APIFL | P01504 | apis florea |
| 624 | 22 | 23.4 | 26 | 1 | MGN_CHICK | P50594 | gallus gall |
| 625 | 22 | 23.4 | 26 | 1 | RBL_VICFA | P05699 | vicia faba |
| 626 | 22 | 23.4 | 26 | 2 | Q4XDG9_PLACH | Q4xdg9 | plasmodium |
| 627 | 22 | 23.4 | 26 | 2 | Q4XIE0_PLACH | Q4xie0 | plasmodium |
| 628 | 22 | 23.4 | 26 | 2 | Q4XM72_PLACH | Q4xm72 | plasmodium |
| 629 | 22 | 23.4 | 26 | 2 | Q4XMQ5_PLACH | Q4xmq5 | plasmodium |
| 630 | 22 | 23.4 | 26 | 2 | Q4XRY4_PLACH | Q4xry4 | plasmodium |
| 631 | 22 | 23.4 | 26 | 2 | Q4YT83_PLABE | Q4yt83 | plasmodium |
| 632 | 22 | 23.4 | 26 | 2 | Q4Z6G9_PLABE | Q4z6g9 | plasmodium |
| 633 | 22 | 23.4 | 26 | 2 | Q9T0Q6_LAMBD | Q9t0q6 | bacteriopha |
| 634 | 22 | 2 | | | | | |

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_813_831
Perfect score: 94
Sequence: 1 ASLKDALLKYIYDNRGTLI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 94 | 100.0 | 19 | 9 | ADW11067 | Adw11067 Clostridi |
| 2 | 94 | 100.0 | 27 | 9 | ADW11117 | Adw11117 Clostridi |
| 3 | 47 | 50.0 | 27 | 9 | ADW11118 | Adw11118 Clostridi |
| 4 | 38 | 40.4 | 30 | 9 | AEC96081 | Aec96081 TccC3 fra |
| 5 | 38 | 40.4 | 30 | 9 | AEC96090 | Aec96090 TccC3 fra |
| 6 | 38 | 40.4 | 30 | 9 | AEC96094 | Aec96094 TccC3 fra |
| 7 | 38 | 40.4 | 30 | 9 | AEC96087 | Aec96087 TccC3 fra |
| 8 | 38 | 40.4 | 30 | 9 | AEC96084 | Aec96084 TccC3 fra |
| 9 | 36 | 38.3 | 17 | 7 | ADE01171 | Ade01171 |

```
RESULT 43
US-08-213-124-9
; Sequence 9, Application US/08213124
; Patent No. 5693325
; GENERAL INFORMATION:
;    APPLICANT:  Kahn, Michael
;    TITLE OF INVENTION:  PEPTIDE VACCINES AND METHODS RELATING
;    TITLE OF INVENTION:  THERETO
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/213,124
;      FILING DATE:  15-MAR-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hermanns, Karl R.
;      REGISTRATION NUMBER:  33,507
;      REFERENCE/DOCKET NUMBER:  670063.411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;      TELEX:  3723836 SEEDANDBERRY
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-213-124-9

  Query Match             30.9%;  Score 29;  DB 1;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 3.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 DNRGTLI 19
              |:|||:|
Db          7 DHRGTII 13
```

```
RESULT 1
H64640
hypothetical protein HP0968 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: H64640
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64640
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-21
A;Cross-references: UNIPROT:O25621; UNIPARC:UPI00000C07B7; GB:AE000605; GB:AE000511; N

  Query Match             33.0%;  Score 31;  DB 2;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 LKDALLKY 10
              |||||: |
Db         12 LKDALIDY 19
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RESULT 12
Q8ZL14_SALTY
ID   Q8ZL14_SALTY   PRELIMINARY;   PRT;    29 AA.
AC   Q8ZL14;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Conserved protein in the LexA regulon.
GN   Name=ysdB; OrderedLocusNames=STM3797.2; ORFNames=STM3796B;
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AE008877; AAL22656.1; -; Genomic_DNA.
DR   BioCyc; STYP99287:STM3796B-MONOMER; -.
KW   Complete proteome.
SQ   SEQUENCE   29 AA;  3211 MW;  9A3B645EB233E781 CRC64;

  Query Match             33.0%;  Score 31;  DB 2;  Length 29;
  Best Local Similarity   66.7%;  Pred. No. 2.6e+03;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 LKDALLKYI 11
              | ||:|||:
Db         20 LLDAVLKYL 28
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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_981_999
Perfect score: 98
Sequence: 1 GEIIWTLQDTQEIKQRVVF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 98 | 100.0 | 19 | 9 | ADW11079 | Adw11079 Clostridi |
| 2 | 74 | 75.5 | 19 | 9 | ADZ69820 | Adz69820 Botulinum |
| 3 | 40 | 40.8 | 19 | 7 | ADF14824 | Adf14824 SLE/sjogr |
| 4 | 38 | 38.8 | 15 | 6 | ABR38942 | Abr38942 HPV-16 E2 |
| 5 | 37.5 | 38.3 | 14 | 4 | ABB56643 | Abb56643 Human SNP |
| 6 | 36 | 36.7 | 12 | 2 | AAR91293 | Aar91293 Anti-idio |
| 7 | 36 | 36.7 | 15 | 6 | ABR38932 | Abr38932 HPV-11 E2 |
| 8 | 36 | 36.7 | 15 | 9 | AEC98599 | Aec98599 HLA-DR bi |
| 9 | 36 | 36.7 | 15 | 9 | AEC98632 | Aec98632 HLA-DR bi |

```
RESULT 4
ABR38942
ID   ABR38942 standard; protein; 15 AA.
XX
AC   ABR38942;
XX
DT   10-MAY-2003  (first entry)
XX
DE   HPV-16 E2 transactivation domain peptide fragment # SEQ ID 22.
XX
KW   Transactivation domain; HPV-11; E2 protein; TAD-inhibitor complex;
KW   binding.
XX
OS   Human papillomavirus.
XX
PN   WO2003006495-A2.
XX
PD   23-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-CA001058.
XX
PR   12-JUL-2001; 2001US-0304412P.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (WANG/) WANG Y.
XX
PI   Cameron DR,  Archambault J,  Yoakim C,  White P;
XX
DR   WPI; 2003-239235/23.
XX
PT   Crystallizable composition comprising papilloma virus E2 transactivation
PT   domain-like polypeptide, complexed with an inhibitor, useful for
PT   providing information about inhibitor-binding pocket of transactivation
PT   domain.
XX
PS   Disclosure; Fig 10; 83pp; English.
XX
CC   The invention relates to a crystallizable composition, comprising a
CC   papilloma virus (PV) E2 transactivation domain (TAD)-like polypeptide
CC   complexed with an inhibitor. Compositions of the invention are useful for
CC   providing useful information on the inhibitor-binding pocket of the
CC   transactivation domain of the HPV-E2 protein. The HPV E2 TAD-inhibitor
CC   crystal structure can be used to identify the residues which are members
CC   of the HPV inhibitor binding pocket and which differ in the CRPV protein.
CC   The current sequence represents the HPV-16 E2 transactivation domain
CC   inhibitor-binding pocket peptide
XX
SQ   Sequence 15 AA;

  Query Match             38.8%;  Score 38;  DB 6;  Length 15;
  Best Local Similarity   87.5%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          3 WTLQDTCE 10
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```
RESULT 7
ABR38932
ID   ABR38932 standard; protein; 15 AA.
XX
AC   ABR38932;
XX
DT   10-MAY-2003  (first entry)
XX
DE   HPV-11 E2 transactivation domain peptide fragment # SEQ ID 12.
XX
KW   Transactivation domain; HPV-11; E2 protein; TAD-inhibitor complex;
KW   binding.
XX
OS   Human papillomavirus.
XX
PN   WO2003006495-A2.
XX
PD   23-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-CA001058.
XX
PR   12-JUL-2001; 2001US-0304412P.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (WANG/) WANG Y.
XX
PI   Cameron DR,  Archambault J,  Yoakim C,  White P;
XX
DR   WPI; 2003-239235/23.
XX
PT   Crystallizable composition comprising papilloma virus E2 transactivation
PT   domain-like polypeptide, complexed with an inhibitor, useful for
PT   providing information about inhibitor-binding pocket of transactivation
PT   domain.
XX
PS   Disclosure; Fig 10; 83pp; English.
XX
CC   The invention relates to a crystallizable composition, comprising a
CC   papilloma virus (PV) E2 transactivation domain (TAD)-like polypeptide
CC   complexed with an inhibitor. Compositions of the invention are useful for
CC   providing useful information on the inhibitor-binding pocket of the
CC   transactivation domain of the HPV-E2 protein. The HPV E2 TAD-inhibitor
CC   crystal structure can be used to identify the residues which are members
CC   of the HPV inhibitor binding pocket and which differ in the CRPV protein.
CC   The current sequence represents the HPV-11 E2 transactivation domain
CC   inhibitor-binding pocket peptide
XX
SQ   Sequence 15 AA;

  Query Match             36.7%;  Score 36;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WTLQDT 10
              ||||||
Db          3 WTLQDT 8
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```
RESULT 24
ADT50360
ID   ADT50360 standard; peptide; 12 AA.
XX
AC   ADT50360;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Human non-muscular type myosin heavy-chain type A peptide Seq 14.
XX
KW   antigen; tumour; cancer; cytoskeletal; myosin;
KW   non-muscular type myosin heavy-chain type A; cytostatic; nmMHC.
XX
OS   Homo sapiens.
XX
PN   WO2004089984-A1.
XX
PD   21-OCT-2004.
XX
PF   03-OCT-2003; 2003WO-JP012732.
XX
PR   04-OCT-2002; 2002JP-00291953.
XX
PA   (MITS-) MITSUBISHI PHARMA CORP.
XX
PI   Hirakawa Y,  Niki H,  Oike S,  Tagawa T,  Hosokawa S,  Yoshiyama Y;
XX
DR   WPI; 2004-757952/74.
XX
PT   New non-muscular type myosin heavy chain type A antigen expressed on cell
PT   surface of tumor mass, useful as target in treatment of cancer such as
PT   stomach cancer.
XX
PS   Example 1; SEQ ID NO 14; 60pp; Japanese.
XX
CC   This invention relates to a novel antigen expressed on the surface of a
CC   cell during formation of a tumour mass. Specifically, it refers to a
CC   labelled ligand that is capable of recognising this antigen and a
CC   pharmaceutical composition derived thereof useful for treating a cancer
CC   patient. The present invention describes the antigen as a cytoskeletal
CC   protein such as myosin or its variant and preferably it is a non-muscular
CC   type myosin heavy-chain type A protein. Accordingly, the pharmaceutical
CC   compositions developed thereof exhibit cytostatic activity and are useful
CC   as anticancer agents in patients expressing this antigen and where the
CC   cancer is chosen from stomach, breast, colon or oesophageal cancer.
CC   Furthermore, the ligand is a monoclonal antibody, preferably a humanised
CC   monoclonal antibody that has cancer reactive properties and as such can
CC   specifically target the cancerous tissue or cell. This peptide sequence
CC   is derived from the human non-muscular type myosin heavy-chain (nmMHC)
CC   type A protein (the antigen), given in an exemplification of the
CC   invention.
XX
SQ   Sequence 12 AA;

  Query Match             32.7%;  Score 32;  DB 8;  Length 12;
  Best Local Similarity   85.7%;  Pred. No. 3.8e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LQDTQEI 13
              |||||| :
Db          6 LQDTQEL 12
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```
RESULT 2
US-09-641-528B-48934
; Sequence 48934, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48934
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-48934

  Query Match             38.8%;  Score 38;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 5e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          1 WTLQDTCE 8
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```
RESULT 3
US-09-641-528B-50061
; Sequence 50061, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50061
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50061

  Query Match             38.8%;  Score 38;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 5e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          1 WTLQDTCE 8
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```
RESULT 4
US-09-641-528B-3817
; Sequence 3817, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3817
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-3817

  Query Match             38.8%;  Score 38;  DB 3;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 7.4;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          1 WTLQDTCE 8
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RESULT 5
US-09-641-528B-7824
; Sequence 7824, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10

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RESULT 22
US-09-641-528B-3714
; Sequence 3714, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3714
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-3714

  Query Match             36.7%;  Score 36;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WTLQDT 10
              ||||||
Db          5 WTLQDT 10
```

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RESULT 25
US-09-641-528B-50612
; Sequence 50612, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50612
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50612

  Query Match             36.7%;  Score 36;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WTLQDT 10
              ||||||
Db          9 WTLQDT 14
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RESULT 1
US-10-715-810-95
; Sequence 95, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 976-994)
US-10-715-810-95

  Query Match             75.5%;  Score 74;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GEIIWTLQDTQEIK 14
              ||||||||||||||
Db          6 GEIIWTLQDTQEIK 19
```

```
RESULT 3
US-10-193-460A-22
; Sequence 22, Application US/10193460A
; Publication No. US20030082769A1
; GENERAL INFORMATION:
;  APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
;  TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS E2 TRANSACTIVATION
;  TITLE OF INVENTION:  DOMAIN/INHIBITOR CO-CRYSTAL AND X-RAY COORDINATES DEFINING
;  TITLE OF INVENTION:  THE INHIBITOR-BINDING POCKET
;  FILE REFERENCE: 13/100
;  CURRENT APPLICATION NUMBER: US/10/193,460A
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: 60/304,412
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: HPV18
US-10-193-460A-22

  Query Match             38.8%;  Score 38;  DB 4;  Length 15;
  Best Local Similarity   87.5%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          3 WTLQDTCE 10
```

```
RESULT 5
US-10-193-460A-12
; Sequence 12, Application US/10193460A
; Publication No. US20030082769A1
; GENERAL INFORMATION:
;  APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
;  TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS E2 TRANSACTIVATION
;  TITLE OF INVENTION:  DOMAIN/INHIBITOR CO-CRYSTAL AND X-RAY COORDINATES DEFINING
;  TITLE OF INVENTION:  THE INHIBITOR-BINDING POCKET
;  FILE REFERENCE: 13/100
;  CURRENT APPLICATION NUMBER: US/10/193,460A
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: 60/304,412
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: HPV11
US-10-193-460A-12

  Query Match             36.7%;  Score 36;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WTLQDT 10
              ||||||
Db          3 WTLQDT 8
```

```
RESULT 19
US-10-530-171-14
; Sequence 14, Application US/10530171
; Publication No. US20060057147A1
; GENERAL INFORMATION:
;  APPLICANT: HIRAKAWA, Youko
;  APPLICANT:  NIKI, Hisae
;  APPLICANT:  OIKE, Shinsuke
;  APPLICANT:  TAGAWA, Toshiaki
;  APPLICANT:  HOSOKAWA,Saiko
;  APPLICANT:  YOSHIYAMA, Yoshiko
;  TITLE OF INVENTION: Antibody recognizing antigen
;  FILE REFERENCE: 235054
;  CURRENT APPLICATION NUMBER: US/10/530,171
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/JP2003/012732
;  PRIOR FILING DATE: 2003-10-03
;  PRIOR APPLICATION NUMBER: JP 2002-291953
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-530-171-14

  Query Match             32.7%;  Score 32;  DB 5;  Length 12;
  Best Local Similarity   85.7%;  Pred. No. 2.9e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LQDTQEI 13
              ||||||:
Db          6 LQDTQEL 12
```

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DT   16-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   13-OCT-1994  (first entry)
XX
DE   Rat HCNP precursor internal fragment #9.
XX
KW   Rat hippocampal cholinergic neurotrophic peptide; rat HCNP;
KW   nerve degeneration; acetylcholine synthesis; neurostimulation.
XX
OS   Rattus norvegicus; (Wistar).
XX
PN   WO9405788-A1.
XX
PD   17-MAR-1994.
XX
PF   27-AUG-1993;   93WO-JP001214.
XX
PR   28-AUG-1992;   92JP-00254170.
PR   29-AUG-1992;   92JP-00253734.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (YAMA/) YAMAMOTO M.
XX
PI   Ojika K,  Tohdoh N,  Tojo S,  Kojima S,  Fukushima N,  Irie T,  Ono K;
PI   Agui H,  Ueki Y,  Nishihara T,  Kamikawa Y,  Taiji M;
XX
DR   WPI; 1994-101193/12.
XX
PT   Neurotrophic peptide(s), precursors and genes - used to treat nervous
PT   degeneration, increases acetylcholine synthesis.
XX
PS   Example 9; Page 161; 200pp; Japanese.
XX
CC   The rat hippocampal cholinergic neurotrophic peptide precursor was
CC   digested by lysyl endopeptidase and the resultant peptide fragments were
CC   sequenced. Peptide AAR49954 is an internal fragment. (Updated on 25-MAR-
CC   2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 28 AA;

  Query Match             32.1%;  Score 36;  DB 2;  Length 28;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 HRYIWI 19
              |||:|:
Db          5 HRYVWL 10
```

```
RESULT 6
US-08-403-378B-10
; Sequence 10, Application US/08403378B
; Patent No. 5759991
;  GENERAL INFORMATION:
;    APPLICANT:  TOHDOH, NAOKI
;    APPLICANT:  TOJO, SHIN-ICHIRO
;    APPLICANT:  KOJIMA, SHIN-ICHI
;    APPLICANT:  UEKI, YASUYUKI
;    APPLICANT:  NISHIHARA, TOSHIO
;    APPLICANT:  FUKUSHIMA, NOBUYUKI
;    APPLICANT:  IRIE, TSUNEMASA
;    APPLICANT:  ONO, KEIICHI
;    APPLICANT:  AGUI, HIDEO
;    APPLICANT:  OJIKA, KOSEI
;    TITLE OF INVENTION:  NEUROTROPHIC PEPTIDE DERIVATIVES
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 PENNSYLVANIA AVENUE, NW
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,378B
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-124688
;      FILING DATE:  27-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-080398
;      FILING DATE:  30-MAR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-280590
;      FILING DATE:  27-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-333241
;      FILING DATE:  21-DEC-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-243003
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/758,043
;      FILING DATE:  12-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/873,764
;      FILING DATE:  27-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/01214
;      FILING DATE:  27-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BIGGART, WADDELL A
;      REGISTRATION NUMBER:  24,861
;      REFERENCE/DOCKET NUMBER:
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  rattus norvegicus
;      STRAIN:  Wistar
;      TISSUE TYPE:  hippocampal tissue of brain
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..28
US-08-403-378B-10

  Query Match             32.1%;  Score 36;  DB 1;  Length 28;
  Best Local Similarity   66.7%;  Pred. No. 46;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 HRYIWI 19
              |||:|:
Db          5 HRYVWL 10
```

```
RESULT 28
US-10-776-521B-280
; Sequence 280, Application US/10776521B
; Publication No. US20050202033A1
; GENERAL INFORMATION:
;  APPLICANT: Fletchner, Jessica
;  APPLICANT:  Prince-Cohane, Kenya
;  APPLICANT:  Mehta, Sunil
;  APPLICANT:  Slusarewicz, Paul
;  APPLICANT:  Andjelic, Sofija
;  APPLICANT:  Barber, Brian
;  TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
;  TITLE OF INVENTION:  IMMUNOTHERAPIES
;  FILE REFERENCE: 8449-405-999
;  CURRENT APPLICATION NUMBER: US/10/776,521B
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: 60/503,417
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: 60/463,746
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 60/462,469
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/447,142
;  PRIOR FILING DATE: 2003-02-13
;  NUMBER OF SEQ ID NOS: 419
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 280
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heat shock protein binding domain with a terminal
;   OTHER INFORMATION: Trp residue
US-10-776-521B-280

  Query Match             29.5%;  Score 33;  DB 5;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.9e+06;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 THRYIW 18
               |||::|
Db           3 THRWLW 8
```

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_1051_1069
Perfect score: 112
Sequence: 1 NNIMFKLDGCRDTHRYIWI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 112 | 100.0 | 19 | 9 | ADW11084 | Adw11084 Clostridi |

RESULT 4
A25310
alpha-amylase/trypsin inhibitor CM1 - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 31-Dec-2004
C;Accession: A25310
R;Barber, D.; Sanchez-Monge, R.; Garcia-Olmedo, F.; Salcedo, G.; Mendez, E.
Biochim. Biophys. Acta 873, 147-151, 1986
A;Title: Evolutionary implications of sequential homologies among members of the tryps
A;Reference number: A90661
A;Accession: A25310
A;Molecule type: protein
A;Residues: 1-28
A;Cross-references: UNIPROT:P16850; UNIPARC:UPI00001763DE
A;Experimental source: cv. Candeal
C;Superfamily: alpha-amylase/trypsin inhibitor
C;Keywords: alpha-amylase inhibitor

Query Match 25.0%; Score 28; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 7.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 LDGCRD 12
              |:|||:
Db         16 LEGCRE 21
```

```
RESULT 49
Q57YV8_HUMAN
ID   Q57YV8_HUMAN   PRELIMINARY;   PRT;    17 AA.
AC   Q57YV8;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein TPO (Fragment).
GN   Name=TPO;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.H.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.K.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AC141930; AAX82037.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   17 AA;  1896 MW;  51C4B9D9295ACAB2 CRC64;

  Query Match             25.9%;  Score 29;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 RDTHR 15
              |||||
Db          8 RDTHR 12
```

```
RESULT 26
ADR46808
ID   ADR46808 standard; peptide; 21 AA.
XX
AC   ADR46808;
XX
DT   04-NOV-2004  (first entry)
XX
DE   H. influenzae hap protein conserved peptide #33.
XX
KW   immunostimulant; antibacterial; vaccine; adhesion; penetration;
KW   immunogenic; Haemophilus infection; hap.
XX
OS   Haemophilus influenzae.
XX
PN   US2004157241-A1.
XX
PD   12-AUG-2004.
XX
PF   15-OCT-2003; 2003US-00687046.
XX
PR   25-AUG-1994;   94US-00296791.
PR   20-APR-2001; 2001US-00839996.
PR   22-FEB-2002; 2002US-00080505.
XX
PA   (SGEM/) ST GEME J W.
XX
PI   St Geme JW;
XX
DR   WPI; 2004-592770/57.
XX
PT   New Haemophilus adhesion and penetration protein, useful for inducing an
PT   immune response against Haemophilus infection and for treating and
PT   preventing Haemophilus infection.
XX
PS   Disclosure; SEQ ID NO 50; 144pp; English.
XX
CC   The invention relates to a recombinant Haemophilus adhesion and
CC   penetration protein. The recombinant Haemophilus adhesion and penetration
CC   protein, nucleic acid, methods, composition, antibodies and vaccines are
CC   useful for inducing an immune response against Haemophilus infection and
CC   for treating and preventing Haemophilus infection. The present sequence
CC   represents the amino acid sequence of an H. influenzae hap protein
CC   conserved peptide.
XX
SQ   Sequence 21 AA;

  Query Match             30.8%;  Score 32;  DB 8;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 6.2e+02;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YVDVNNVGIR 11
              ||||:|  ::
Db          8 YVDVSNANVQ 17
```

```
RESULT 6
US-10-080-505-50
; Sequence 50, Application US/10080505
; Patent No. 6676948
; GENERAL INFORMATION:
;  APPLICANT: St. Geme, Joseph W.
;  TITLE OF INVENTION: HAEMOPHILUS ADHERENCE AND PENETRATION PROTIENS
;  FILE REFERENCE: A-59941-1/RFT/DCF/DHR
;  CURRENT APPLICATION NUMBER: US/10/080,505
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: US 08/296,791
;  PRIOR FILING DATE: 1994-10-25
;  PRIOR APPLICATION NUMBER: US 09/839,996
;  PRIOR FILING DATE: 2001-04-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Haemophilus influenzae
US-10-080-505-50

  Query Match             30.8%;  Score 32;  DB 2;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YVDVNNVGIR 11
              ||||:|  ::
Db          8 YVDVSNANVQ 17
```

```
RESULT 22
US-09-068-804-28
; Sequence 28, Application US/09068804
; Patent No. 6861247
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Samuel I.
;    TITLE OF INVENTION:  SALMONELLA SECRETED PROTEINS
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,804
;      FILING DATE:  14-MAY-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/18504
;      FILING DATE:  14-NOV-1996
;      APPLICATION NUMBER:  60/006,733
;      FILING DATE:  14-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/292002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-068-804-28

  Query Match             28.8%;  Score 30;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 VNNVGIRGYMYL 16
              ::|||||    ||
Db          3 ISNVGINPAAYL 14
```

```
RESULT 23
US-09-068-804-30
; Sequence 30, Application US/09068804
; Patent No. 6861247
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Samuel I.
;    TITLE OF INVENTION:  SALMONELLA SECRETED PROTEINS
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,804
;      FILING DATE:  14-MAY-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/18504
;      FILING DATE:  14-NOV-1996
;      APPLICATION NUMBER:  60/006,733
;      FILING DATE:  14-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/292002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-068-804-30

  Query Match             28.8%;  Score 30;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 VNNVGIRGYMYL 16
              ::||||    ||
Db          3 ISNVGINPAAYL 14
```

```
 Sequence 59, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
;  APPLICANT: Neben, Steven
;  APPLICANT:  Takeuchi, Toshihiko
;  APPLICANT:  Tomkinson, Adrian
;  TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
;  TITLE OF INVENTION:  Treatment Of Asthma
;  FILE REFERENCE: 7430*163
;  CURRENT APPLICATION NUMBER: US/10/320,231A
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/342,174
;  PRIOR FILING DATE: 2001-12-17
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic sequence
US-10-320-231A-59

  Query Match             28.8%;  Score 30;  DB 4;  Length 11;
  Best Local Similarity   83.3%;  Pred. No. 5.8e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GIRGYM 14
              |||||:
Db          5 GIRGYL 10
```

```
Sequence 506, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
;  APPLICANT: EDWARDS, ALED
;  APPLICANT:  DHARAMSI, AKIL
;  APPLICANT:  VEDADI, MASOUD
;  TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
;  FILE REFERENCE: IPT-330.01
;  CURRENT APPLICATION NUMBER: US/11/122,986
;  CURRENT FILING DATE:  2005-05-05
;  PRIOR APPLICATION NUMBER: 60/423,875
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,832
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,915
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,757
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,758
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/424,367
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,376
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,370
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,362
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,373
;  PRIOR FILING DATE: 2002-11-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 844
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 506
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-11-122-986-506

  Query Match             26.0%;  Score 27;  DB 7;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 MYLKGP 19
               :||:||
Db           2 LYLQGP 7
```

```
 Sequence 353, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
;  APPLICANT: Kundig, Thomas M.
;  APPLICANT:  Simard, John J. L.
;  TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
;  FILE REFERENCE: MANNK.001CP2C1
;  CURRENT APPLICATION NUMBER: US/11/313,152
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/776,232
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 09/380,534
;  PRIOR FILING DATE: 1999-09-01
;  PRIOR APPLICATION NUMBER: PCT/US98/14289
;  PRIOR FILING DATE: 1998-07-10
;  PRIOR APPLICATION NUMBER: 08/988,320
;  PRIOR FILING DATE: 1997-12-10
;  PRIOR APPLICATION NUMBER: CA 2,209,815
;  PRIOR FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 569
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Haemophilus influenzae
US-11-313-152-353

  Query Match             25.0%;  Score 26;  DB 7;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 RGYMY 15
               |||:|
Db           1 RGYVY 5
```

```
RESULT 48
US-11-409-939-38
; Sequence 38, Application US/11409939
; Publication No. US20060240018A1
;   GENERAL INFORMATION:
;        APPLICANT: Koieda, Shohei
;        TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
;        NUMBER OF SEQUENCES: 118
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
;             STREET: 121 South Eighth Street, Ste. 1600
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/409,939
;             FILING DATE: 24-Apr-2006
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/096,749
;             FILING DATE: June 12, 1998
;             APPLICATION NUMBER:
;             FILING DATE:
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ann S. Viksnins
;             REGISTRATION NUMBER: 37,748
;             REFERENCE/DOCKET NUMBER: 109.034US1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6900
;             TELEFAX: (612) 339-3061
;   INFORMATION FOR SEQ ID NO: 38:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 7 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: internal
;        ORIGINAL SOURCE:
;        SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-11-409-939-38

  Query Match             24.0%;  Score 25;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 3e+05;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 RGYMYL 16
               ||:|:|
Db           1 RGFMWL 6
```

```
RESULT 4
B85928
hypothetical protein Z4088 [imported] - Escherichia coli (strain O157:H7, substrain ED
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85928
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25
A;Cross-references: UNIPROT:Q8X3V1; UNIPARC:UPI00000D0EA3; GB:AE005174; NID:g12517242;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4088

  Query Match             26.0%;  Score 27;  DB 2;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 6.8e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GIRGYM 14
              |:|||:
Db         14 GLRGYV 19
```

```
RESULT 4
Q6R273_LACLC
ID   Q6R273_LACLC   PRELIMINARY;   PRT;    12 AA.
AC   Q6R273;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   ArgC (Fragment).
GN   Name=argC;
OS   Lactococcus lactis subsp. cremoris (Streptococcus cremoris).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1359;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MG1363;
RX   PubMed=14762010; DOI=10.1128/JB.186.4.1147-1157.2004;
RA   Larsen R., Buist G., Kuipers O.P., Kok J.;
RT   "ArgR and AhrC are both required for regulation of arginine metabolism
RT   in Lactococcus lactis.";
RL   J. Bacteriol. 186:1147-1157(2004).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY518514; AAR99645.1; -; Genomic_DNA.
FT   NON_TER      12      12
SQ   SEQUENCE   12 AA;  1335 MW;  CC8E9BF86162C05D CRC64;

  Query Match             30.8%;  Score 32;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VGIRGY 13
              ||||||
Db          7 VGIRGY 12
```

```
RESULT 6
Q9GLI9_PIG
ID   Q9GLI9_PIG     PRELIMINARY;   PRT;    21 AA.
AC   Q9GLI9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Leucine aminopeptidase (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Simmen F.A.,
RA   Rexroad C.E. III, Keele J.W.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF267719; AAG25934.1; -; Genomic_DNA.
DR   HSSP; P00727; 1LAM.
DR   MEROPS; M17.005; -.
DR   GO; GO:0004177; F:aminopeptidase activity; IEA.
KW   Aminopeptidase.
FT   NON_TER       1      1
FT   NON_TER      21     21
SQ   SEQUENCE   21 AA;  2198 MW;  7C2EF81999015E1F CRC64;

  Query Match             29.8%;  Score 31;  DB 2;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.4e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DVNNVG 9
              ||||:|
Db          7 DVNNIG 12
```

```
RESULT 42
Q8X3V1_ECO57
ID   Q8X3V1_ECO57   PRELIMINARY;   PRT;    25 AA.
AC   Q8X3V1;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   No significant matches.
GN   OrderedLocusNames=z4088;
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX   MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AE005174; AAG57886.1; -; Genomic_DNA.
DR   PIR; B85928; B85928.
KW   Complete proteome.
SQ   SEQUENCE   25 AA;  3152 MW;  0C2F84A4E0257B77 CRC64;

  Query Match             26.0%;  Score 27;  DB 2;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 7.9e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GIRGYM 14
              |:|||:
Db         14 GLRGYV 19
```

```
RESULT 23
ABO12635
ID   ABO12635 standard; peptide; 25 AA.
XX
AC   ABO12635;
XX
DT   25-AUG-2003  (first entry)
XX
DE   Human zinc finger DNA binding domain #934.
XX
KW   Composite binding polypeptide; zinc finger nucleic acid binding domain;
KW   autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO200299084-A2.
XX
PD   12-DEC-2002.
XX
PF   04-APR-2002; 2002WO-US022272.
XX
PR   04-APR-2001; 2001GB-00008491.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Moore M,  Sepp A,  Isalan M,  Choo Y;
XX
DR   WPI; 2003-278214/27.
XX
PT   New composite binding zinc finger polypeptide, useful for designing
PT   sequence-specific binding proteins regulating gene expression in the
PT   fields of molecular biology, and for the diagnosis and treatment of
PT   autoimmune disorders.
XX
PS   Example 2; Page 91; 157pp; English.
XX
CC   The invention relates to a composite binding polypeptide comprising a
CC   first natural binding domain derived from a first natural binding
CC   polypeptide and a second natural binding domain derived from a second
CC   natural binding polypeptide, where the first and second natural binding
CC   polypeptides may be the same or different and where the polypeptide binds
CC   to a target differing from the natural target of both the first and
CC   second binding polypeptides. The invention also relates to a chimeric
CC   polypeptide comprising a binding polypeptide cited above and a biological
CC   effector domain, a library of natural binding domains, a library of
CC   natural zinc finger nucleic acid binding domains comprising a linker
CC   attached to it, a method for selecting a binding polypeptide capable of
CC   binding to a target site and a method for designing a composite binding
CC   polypeptide. The methods and compositions of the present invention are
CC   useful for designing sequence-specific binding proteins for regulation of
CC   gene expression in the fields of molecular biology. They can also be used
CC   for the diagnosis and treatment of autoimmune disorders, and as research
CC   tools and in transgenic animals. This sequence represents a human zinc
CC   finger DNA binding domain used in the scope of the invention
XX
SQ   Sequence 25 AA;

  Query Match             30.8%;  Score 40;  DB 6;  Length 25;
  Best Local Similarity   54.5%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          5 GCSWEFIPVDD 15
              ||||:|   |:
Db          7 GCSWKFARSDE 17
```

RESULT 1
US-[redacted]
; Sequence 105, Application US[redacted]
; Publication No. US20050106182A1
; GENERAL INFORMATION:
; APPLICANT: Li, Shengwen
; APPLICANT: Kei, Aoki R.
; TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
; FILE REFERENCE: ALLE0004-100
; CURRENT APPLICATION NUMBER: US[redacted]
; CURRENT FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment (residues 1277-1296)
US-10-715-810-105

1275-1296

Query Match 93.1%; Score 121; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 TLGCSWEFIPVDDGWGERPL 22
              ||||||||||||||||||||
Db          1 TLGCSWEFIPVDDGWGERPL 20
```

```
RESULT 37
US-10-732-620-9
; Sequence 9, Application US/10732620
; Publication No. US20050032186A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jin-Soo
;  APPLICANT:  Shin, Hyun-Chul
;  APPLICANT:  Kwon, Heung-Sun
;  TITLE OF INVENTION: REGULATORY ZINC FINGER PROTEINS
;  FILE REFERENCE: 12279-009001
;  CURRENT APPLICATION NUMBER: US/10/732,620
;  CURRENT FILING DATE:  2003-12-09
;  PRIOR APPLICATION NUMBER: US 60/431,892
;  PRIOR FILING DATE: 2002-12-09
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 25
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-620-9

  Query Match             28.5%;  Score 37;  DB 5;  Length 25;
  Best Local Similarity   45.5%;  Pred. No. 5.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCSWEFIPVDD 15
              ||:|:|   |:
Db          7 GCTWKFARSDE 17


RESULT 38
```

```
Sequence 92, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
;  APPLICANT: Parekh, Rajesh
;  TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
;  TITLE OF INVENTION:  SCHIZOPHRENIA
;  FILE REFERENCE: 9195-061-999
;  CURRENT APPLICATION NUMBER: US/09/791,378
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/750,395
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 677
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-378-92

  Query Match             27.7%;  Score 36;  DB 3;  Length 14;
  Best Local Similarity   66.7%;  Pred. No. 4.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 IPVDDGWGE 19
              ||::|| ||
Db          1 IPIEDGSGE 9
```

ADV55232
ID ADV55232 standard; peptide; 14 AA.
XX
AC ADV55232;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 2729.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 2729; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 14 AA;

```
  Query Match             37.4%;  Score 37;  DB 9;  Length 14;
  Best Local Similarity   66.7%;  Pred. No. 68;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EENISLDLI 9
              |||::|||:
Db          4 EENVTLDLV 12
```

```
RESULT 19
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental aller
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11
A;Cross-references: UNIPARC:UPI000017C9F3
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

  Query Match             24.2%;  Score 24;  DB 2;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 8.1e+02;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 SLDLIQQ 11
              |:||::|
Db          5 SMDLMEQ 11
```

```
RESULT 20
S41601
interferon alpha receptor 1 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C;Accession: S41601
R;Abramovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.
FEBS Lett. 338, 295-300, 1994
A;Title: Identification of mRNAs encoding two different soluble forms of the human int
A;Reference number: S41601; MUID:94139943; PMID:8307198
A;Accession: S41601
A;Molecule type: mRNA
A;Residues: 1-14
A;Cross-references: UNIPARC:UPI000017C27A
C;Keywords: cytokine receptor

  Query Match             24.2%;  Score 24;  DB 2;  Length 14;
  Best Local Similarity   83.3%;  Pred. No. 1.1e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ENISLD 7
              |||||:
Db          7 ENISLN 12
```

```
RESULT 43
S38527
rRNA N-glycosidase (EC 3.2.2.22) saporin S6 - common soapwort (fragment)
C;Species: Saponaria officinalis (common soapwort)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Jul-1998
C;Accession: S38527
R;Ferreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; R
Biochim. Biophys. Acta 1216, 31-42, 1993
A;Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRN
A;Reference number: S38521; MUID:94032486; PMID:8218413
A;Accession: S38527
A;Molecule type: protein
A;Residues: 1-30
A;Cross-references: UNIPARC:UPI0000174670
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycosidase; hydrolase

  Query Match             23.2%;  Score 23;  DB 2;  Length 30;
  Best Local Similarity   57.1%;  Pred. No. 3.5e+03;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NISLDLI 9
              :|:|||:
Db          3 SITLDLV 9
```

```
B61497
seed protein ws-17 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: B61497
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-d
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: B61497
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12
A;Cross-references: UNIPROT:Q7M1H9; UNIPARC:UPI000017B06B
C;Keywords: seed

  Query Match             22.2%;  Score 22;  DB 2;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 LTFNFD 19
              ::|||:
Db          3 ISFNFN 8
```

PA0007
lectin B1 - Psophocarpus scandens (fragment)
C;Species: Psophocarpus scandens
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: PA0007
R;Kortt, A.A.
Phytochemistry 27, 2847-2855, 1988
A;Title: Isolation and characterization of the lectins from the seeds of Psophocarpus
A;Reference number: PA0005
A;Accession: PA0007
A;Molecule type: protein
A;Residues: 1-14
A;Cross-references: UNIPROT:P22584; UNIPARC:UPI000012E3DA
A;Experimental source: seed
C;Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can
C;Keywords: lectin

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  Matches  3;  Conservative  3;  Mismatches  0;  Indels  0;  Gaps  0;

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Db          3 ISFNFN 8
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 Sequence 225, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas C
;  APPLICANT:  Wild, Kenneth D
;  APPLICANT:  Sitney, Karen C
;  APPLICANT:  Min, Hosung
;  APPLICANT:  Kimmel, Bruce
;  TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Facto
;  FILE REFERENCE: A-827US
;  CURRENT APPLICATION NUMBER: US/10/666,480
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: 60/412,524
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Therapeutically active peptide of randomly generated,  non-natu
;   OTHER INFORMATION: lly occurring sequence
US-10-666-480-225

  Query Match             31.3%;  Score 31;  DB 4;  Length 26;
  Best Local Similarity   55.6%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          9 SLPLVEQYF 17
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Sequence 178, Application US/10948707
; Publication No. US20050187147A1
; GENERAL INFORMATION:
;  APPLICANT: Ballatore, Carlo
;  APPLICANT:  Castellino, Angelo
;  APPLICANT:  Desharnais, Joel
;  APPLICANT:  Guo, Zijian
;  APPLICANT:  Li, Qing
;  APPLICANT:  Newman, Michael James
;  APPLICANT:  Sun, Chengzao
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;  TITLE OF INVENTION:  DRUG EFFICIENCY
;  FILE REFERENCE: 17967-003001
;  CURRENT APPLICATION NUMBER: US/10/948,707
;  CURRENT FILING DATE:  2004-09-22
;  PRIOR APPLICATION NUMBER: 60/505,325
;  PRIOR FILING DATE: 2003-09-22
;  PRIOR APPLICATION NUMBER: 60/568,340
;  PRIOR FILING DATE: 2004-05-04
;  PRIOR APPLICATION NUMBER: 60/581,835
;  PRIOR FILING DATE: 2004-06-22
;  NUMBER OF SEQ ID NOS: 1422
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-948-707-178

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  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EENVSVD 7
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Sequence 225, Application US/10666480
; Patent No. 6919426
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas C
;  APPLICANT:  Wild, Kenneth D
;  APPLICANT:  Sitney, Karen C
;  APPLICANT:  Min, Hosung
;  APPLICANT:  Kimmel, Bruce
;  TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Facto
;  FILE REFERENCE: A-827US
;  CURRENT APPLICATION NUMBER: US/10/666,480
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: 60/412,524
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Therapeutically active peptide of randomly generated,  non-natu
;   OTHER INFORMATION: lly occurring sequence
US-10-666-480-225

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Db          9 SLPLVEQYF 17
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Sequence 57, Application US/08188583
; Patent No. 5851813
;  GENERAL INFORMATION:
;    APPLICANT:  Desrosiers, Ronald C.
;    TITLE OF INVENTION:  PRIMATE LENTIVIRUS VACCINES
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/188,583
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/727,494
;      FILING DATE:  July 9, 1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/551,945
;      FILING DATE:  July 12, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  Reg. No. 5851813 29,066
;      REFERENCE/DOCKET NUMBER:  00246/079002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-188-583-57

  Query Match             28.3%;  Score 28;  DB 1;  Length 13;
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Qy         10 QQYYLTF 16
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Db          3 EEHYLTF 9
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# SCORE Search Results Details for Application 10821669 and Search Result us-10-821-669-1_copy_519_537.szlm30.rag.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10821669 and Search Result us-10-821-669-1_copy_519_537.szlm30.rag.

start

Go Back to previous page

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_519_537
Perfect score: 94
Sequence: 1 NLSSDIIGQLELMPNIERF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 94 | 100.0 | 27 | 9 | ADW11104 | Adw11104 Clostridi |
| 3 | 47 | 50.0 | 27 | 9 | ADW11105 | Adw11105 Clostridi |
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| 164 | 28 | 29.8 | 9 | 7 | ADE68697 | Ade68697 Human 161 |
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| 166 | 28 | 29.8 | 9 | 7 | ADE68916 | Ade68916 Human 161 |
| 167 | 28 | 29.8 | 9 | 7 | ADE66509 | Ade66509 Human 161 |
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| 174 | 28 | 29.8 | 9 | 7 | ADE66746 | Ade66746 Human 161 |
| 175 | 28 | 29.8 | 9 | 7 | ADE66240 | Ade66240 Human 161 |
| 176 | 28 | 29.8 | 9 | 7 | ADE66487 | Ade66487 Human 161 |
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| 185 | 28 | 29.8 | 10 | 7 | ADE66856 | Ade66856 Human 161 |
| 186 | 28 | 29.8 | 10 | 7 | ADE69292 | Ade69292 Human 161 |
| 187 | 28 | 29.8 | 10 | 7 | ADE69249 | Ade69249 Human 161 |
| 188 | 28 | 29.8 | 10 | 7 | ADE67367 | Ade67367 Human 161 |
| 189 | 28 | 29.8 | 10 | 7 | ADE69899 | Ade69899 Human 161 |
| 190 | 28 | 29.8 | 10 | 7 | ADE66892 | Ade66892 Human 161 |
| 191 | 28 | 29.8 | 10 | 7 | ADE66384 | Ade66384 Human 161 |
| 192 | 28 | 29.8 | 10 | 7 | ADE66679 | Ade66679 Human 161 |
| 193 | 28 | 29.8 | 10 | 7 | ADE67108 | Ade67108 Human 161 |
| 194 | 28 | 29.8 | 10 | 7 | ADE69652 | Ade69652 Human 161 |
| 195 | 28 | 29.8 | 11 | 2 | AAR66883 | Aar66883 Agonist p |
| 196 | 28 | 29.8 | 11 | 2 | AAW01916 | Aaw01916 C140 rece |
| 197 | 28 | 29.8 | 11 | 7 | ADD23033 | Add23033 Breast ca |
| 198 | 28 | 29.8 | 12 | 3 | AAY84189 | Aay84189 Amino aci |
| 199 | 28 | 29.8 | 12 | 8 | ADO24729 | Ado24729 Mouse lep |
| 200 | 28 | 29.8 | 13 | 5 | ABP63630 | Abp63630 Human MHC |
| 201 | 28 | 29.8 | 13 | 5 | AAE27221 | Aae27221 Human obe |
| 202 | 28 | 29.8 | 15 | 3 | AAY54775 | Aay54775 Human sub |
| 203 | 28 | 29.8 | 15 | 3 | AAY67138 | Aay67138 Human pro |
| 204 | 28 | 29.8 | 15 | 4 | AAU38677 | Aau38677 Human sub |
| 205 | 28 | 29.8 | 15 | 5 | AAO17727 | Aao17727 Human air |
| 206 | 28 | 29.8 | 15 | 5 | ABG91253 | Abg91253 Peptide a |
| 207 | 28 | 29.8 | 15 | 7 | ADE70767 | Ade70767 Human 161 |
| 208 | 28 | 29.8 | 15 | 7 | ADE70471 | Ade70471 Human 161 |
| 209 | 28 | 29.8 | 15 | 7 | ADE70354 | Ade70354 Human 161 |
| 210 | 28 | 29.8 | 15 | 7 | ADE70728 | Ade70728 Human 161 |
| 211 | 28 | 29.8 | 15 | 7 | ADE70110 | Ade70110 Human 161 |
| 212 | 28 | 29.8 | 15 | 7 | ADE70355 | Ade70355 Human 161 |
| 213 | 28 | 29.8 | 15 | 7 | ADE70470 | Ade70470 Human 161 |
| 214 | 28 | 29.8 | 15 | 7 | ADE70504 | Ade70504 Human 161 |
| 215 | 28 | 29.8 | 15 | 7 | ADE70503 | Ade70503 Human 161 |
| 216 | 28 | 29.8 | 15 | 7 | ADE70820 | Ade70820 Human 161 |
| 217 | 28 | 29.8 | 15 | 8 | ADN65557 | Adn65557 HLA bindi |
| 218 | 28 | 29.8 | 15 | 8 | ADT07772 | Adt07772 Salmon ca |
| 219 | 28 | 29.8 | 17 | 4 | AAM52595 | Aam52595 Peptide # |
| 220 | 28 | 29.8 | 17 | 8 | ADV86497 | Adv86497 Parathyro |
| 221 | 28 | 29.8 | 18 | 2 | AAR27585 | Aar27585 TNF bindi |
| 222 | 28 | 29.8 | 18 | 2 | AAW04312 | Aaw04312 Modified |
| 223 | 28 | 29.8 | 18 | 2 | AAW45586 | Aaw45586 Peptide f |
| 224 | 28 | 29.8 | 18 | 3 | AAB19656 | Aab19656 Streptoco |
| 225 | 28 | 29.8 | 18 | 6 | ABG71717 | Abg71717 Antigenic |
| 226 | 28 | 29.8 | 18 | 8 | ADK49420 | Adk49420 Human car |
| 227 | 28 | 29.8 | 18 | 8 | ADV86510 | Adv86510 Parathyro |
| 228 | 28 | 29.8 | 19 | 2 | AAR26823 | Aar26823 Cell adhe |
| 229 | 28 | 29.8 | 20 | 2 | AAR30900 | Aar30900 Cell adhe |
| 230 | 28 | 29.8 | 20 | 2 | AAR92724 | Aar92724 Immunogen |
| 231 | 28 | 29.8 | 20 | 3 | AAB28456 | Aab28456 Murine OB |
| 232 | 28 | 29.8 | 20 | 3 | AAY87734 | Aay87734 Murine OB |
| 233 | 28 | 29.8 | 20 | 3 | AAB28475 | Aab28475 Murine OB |
| 234 | 28 | 29.8 | 20 | 5 | ABG66603 | Abg66603 IgE Fceps |
| 235 | 28 | 29.8 | 20 | 5 | ABB84124 | Abb84124 Murine Ob |
| 236 | 28 | 29.8 | 20 | 6 | ABP83487 | Abp83487 G protein |
| 237 | 28 | 29.8 | 20 | 6 | ABU64569 | Abu64569 Human obe |
| 238 | 28 | 29.8 | 20 | 8 | ADH15364 | Adh15364 Gliadin r |
| 239 | 28 | 29.8 | 20 | 8 | ADH16095 | Adh16095 Gliadin r |
| 240 | 28 | 29.8 | 20 | 8 | ADH16094 | Adh16094 Gliadin r |

| | | | | | | |
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| 241 | 28 | 29.8 | 20 | 8 | ADH15365 | Adh15365 Gliadin r |
| 242 | 28 | 29.8 | 20 | 8 | ADT93154 | Adt93154 Murine ob |
| 243 | 28 | 29.8 | 20 | 9 | AED19923 | Aed19923 Canine pa |
| 244 | 28 | 29.8 | 20 | 9 | AEE34588 | Aee34588 Wheat gli |
| 245 | 28 | 29.8 | 20 | 9 | AEE34596 | Aee34596 Wheat gli |
| 246 | 28 | 29.8 | 20 | 9 | AEE34589 | Aee34589 Wheat gli |
| 247 | 28 | 29.8 | 20 | 9 | AEE34597 | Aee34597 Wheat gli |
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| 250 | 28 | 29.8 | 20 | 9 | AEE34592 | Aee34592 Wheat gli |
| 251 | 28 | 29.8 | 21 | 4 | ABB42885 | Abb42885 Peptide # |
| 252 | 28 | 29.8 | 21 | 4 | AAM36703 | Aam36703 Peptide # |
| 253 | 28 | 29.8 | 21 | 4 | AAM76594 | Aam76594 Human bon |
| 254 | 28 | 29.8 | 21 | 4 | AAM63781 | Aam63781 Human bra |
| 255 | 28 | 29.8 | 21 | 4 | ABG58294 | Abg58294 Human liv |
| 256 | 28 | 29.8 | 21 | 5 | ABG45836 | Abg45836 Human pep |
| 257 | 28 | 29.8 | 21 | 5 | AAB71448 | Aab71448 Human C3 |
| 258 | 28 | 29.8 | 22 | 2 | AAR99403 | Aar99403 Drosophil |
| 259 | 28 | 29.8 | 22 | 2 | AAW65059 | Aaw65059 E. tenell |
| 260 | 28 | 29.8 | 22 | 5 | AAB71462 | Aab71462 Human C3 |
| 261 | 28 | 29.8 | 24 | 1 | AAP20305 | Aap20305 24 residu |
| 262 | 28 | 29.8 | 24 | 7 | ADE03435 | Ade03435 BGS-2 leu |
| 263 | 28 | 29.8 | 24 | 9 | ADV55692 | Adv55692 G protein |
| 264 | 28 | 29.8 | 24 | 9 | ADV54697 | Adv54697 G protein |
| 265 | 28 | 29.8 | 24 | 9 | ADV55693 | Adv55693 G protein |
| 266 | 28 | 29.8 | 24 | 9 | ADV54696 | Adv54696 G protein |
| 267 | 28 | 29.8 | 25 | 1 | AAP60857 | Aap60857 Sequence |
| 268 | 28 | 29.8 | 25 | 2 | AAW09790 | Aaw09790 Peptide e |
| 269 | 28 | 29.8 | 25 | 5 | ABG62201 | Abg62201 Eubacteri |
| 270 | 28 | 29.8 | 26 | 6 | ABP97145 | Abp97145 C-Myc fra |
| 271 | 28 | 29.8 | 26 | 6 | ABP97144 | Abp97144 C-Myc fra |
| 272 | 28 | 29.8 | 26 | 8 | ADR84079 | Adr84079 S. pyogen |
| 273 | 28 | 29.8 | 27 | 2 | AAW00861 | Aaw00861 Anti-obes |
| 274 | 28 | 29.8 | 27 | 8 | ADK49421 | Adk49421 Human car |
| 275 | 28 | 29.8 | 27 | 9 | ADV44820 | Adv44820 Murine al |
| 276 | 28 | 29.8 | 28 | 1 | AAP82100 | Aap82100 Synthetic |
| 277 | 28 | 29.8 | 28 | 1 | AAP82099 | Aap82099 Synthetic |
| 278 | 28 | 29.8 | 29 | 1 | AAP80525 | Aap80525 Sequence |
| 279 | 28 | 29.8 | 29 | 1 | AAP82107 | Aap82107 Synthetic |
| 280 | 28 | 29.8 | 29 | 1 | AAP82108 | Aap82108 Synthetic |
| 281 | 28 | 29.8 | 29 | 2 | AAR61495 | Aar61495 L-Proline |
| 282 | 28 | 29.8 | 29 | 2 | AAR88115 | Aar88115 L-proline |
| 283 | 28 | 29.8 | 29 | 8 | ABO57855 | Abo57855 Human gen |
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| 286 | 28 | 29.8 | 30 | 1 | AAP40568 | Aap40568 Sequence |
| 287 | 28 | 29.8 | 30 | 1 | AAP82825 | Aap82825 Salmon ca |
| 288 | 28 | 29.8 | 30 | 1 | AAP82741 | Aap82741 Des-19-le |
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| 290 | 28 | 29.8 | 30 | 2 | AAR07951 | Aar07951 Synthetic |
| 291 | 28 | 29.8 | 30 | 2 | AAR07769 | Aar07769 Calcium m |
| 292 | 27 | 28.7 | 8 | 8 | ADS97525 | Ads97525 Human MEP |
| 293 | 27 | 28.7 | 9 | 5 | ABJ01798 | Abj01798 158P1D7 r |
| 294 | 27 | 28.7 | 9 | 5 | ABJ01511 | Abj01511 158P1D7 r |
| 295 | 27 | 28.7 | 9 | 5 | ABJ01313 | Abj01313 158P1D7 r |
| 296 | 27 | 28.7 | 9 | 5 | ABJ01886 | Abj01886 158P1D7 r |
| 297 | 27 | 28.7 | 9 | 6 | ABU76577 | Abu76577 Novel pro |
| 298 | 27 | 28.7 | 10 | 4 | AAG95264 | Aag95264 Human com |
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| 300 | 27 | 28.7 | 10 | 5 | ABJ01461 | Abj01461 158P1D7 r |
| 301 | 27 | 28.7 | 10 | 5 | ABJ01361 | Abj01361 158P1D7 r |

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| 302 | 27 | 28.7 | 10 | 6 | ABU77717 | Abu77717 Novel pro |
| 303 | 27 | 28.7 | 10 | 6 | ABU77793 | Abu77793 Novel pro |
| 304 | 27 | 28.7 | 10 | 6 | ABU75147 | Abu75147 Novel pro |
| 305 | 27 | 28.7 | 10 | 6 | ABU75732 | Abu75732 Novel pro |
| 306 | 27 | 28.7 | 10 | 6 | ABU77848 | Abu77848 Novel pro |
| 307 | 27 | 28.7 | 10 | 6 | ABR01568 | Abr01568 Human ant |
| 308 | 27 | 28.7 | 10 | 8 | ADK03047 | Adk03047 Hepatitis |
| 309 | 27 | 28.7 | 10 | 8 | ADK03072 | Adk03072 Hepatitis |
| 310 | 27 | 28.7 | 13 | 4 | AAU28716 | Aau28716 DPI trypt |
| 311 | 27 | 28.7 | 13 | 4 | AAU28698 | Aau28698 DPI trypt |
| 312 | 27 | 28.7 | 13 | 4 | AAU25223 | Aau25223 Schizophr |
| 313 | 27 | 28.7 | 13 | 4 | AAB87228 | Aab87228 Breast-ca |
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| 315 | 27 | 28.7 | 13 | 4 | AAU26364 | Aau26364 Depressio |
| 316 | 27 | 28.7 | 13 | 4 | AAU15567 | Aau15567 Schizophr |
| 317 | 27 | 28.7 | 13 | 4 | ABB52265 | Abb52265 Human API |
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| 319 | 27 | 28.7 | 13 | 8 | ADN31903 | Adn31903 Human Alz |
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| 321 | 27 | 28.7 | 14 | 1 | AAP94363 | Aap94363 Part of t |
| 322 | 27 | 28.7 | 14 | 8 | ADT39061 | Adt39061 hSARS vir |
| 323 | 27 | 28.7 | 14 | 8 | ADS78481 | Ads78481 SARS viru |
| 324 | 27 | 28.7 | 14 | 8 | ADT36591 | Adt36591 hSARS vir |
| 325 | 27 | 28.7 | 14 | 8 | ABY00094 | Aby00094 SARS coro |
| 326 | 27 | 28.7 | 15 | 6 | ABJ70569 | Abj70569 184P1E2-r |
| 327 | 27 | 28.7 | 15 | 6 | ABJ69983 | Abj69983 184P1E2-r |
| 328 | 27 | 28.7 | 15 | 6 | ABJ71760 | Abj71760 184P1E2-r |
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| 337 | 27 | 28.7 | 15 | 6 | ABJ71479 | Abj71479 184P1E2-r |
| 338 | 27 | 28.7 | 15 | 6 | ABJ69601 | Abj69601 184P1E2-r |
| 339 | 27 | 28.7 | 15 | 6 | ABJ70533 | Abj70533 184P1E2-r |
| 340 | 27 | 28.7 | 15 | 8 | ADP26414 | Adp26414 Plasmodiu |
| 341 | 27 | 28.7 | 17 | 4 | AAB70776 | Aab70776 Human Gra |
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| 343 | 27 | 28.7 | 17 | 9 | ADV12720 | Adv12720 Human pho |
| 344 | 27 | 28.7 | 18 | 8 | ADP21013 | Adp21013 Cottontai |
| 345 | 27 | 28.7 | 18 | 8 | ADP21070 | Adp21070 Plant vir |
| 346 | 27 | 28.7 | 18 | 9 | AEE68112 | Aee68112 Cottontai |
| 347 | 27 | 28.7 | 19 | 6 | ABR62557 | Abr62557 hTid liga |
| 348 | 27 | 28.7 | 19 | 8 | ADG74064 | Adg74064 Cottontai |
| 349 | 27 | 28.7 | 19 | 8 | ADP21069 | Adp21069 Plant vir |
| 350 | 27 | 28.7 | 19 | 9 | AED02396 | Aed02396 Papilloma |
| 351 | 27 | 28.7 | 19 | 9 | AEE68159 | Aee68159 Human imm |
| 352 | 27 | 28.7 | 20 | 4 | AAB74840 | Aab74840 Human min |
| 353 | 27 | 28.7 | 20 | 4 | AAB67252 | Aab67252 Hepatitis |
| 354 | 27 | 28.7 | 20 | 4 | AAM89373 | Aam89373 Human imm |
| 355 | 27 | 28.7 | 20 | 8 | ADU79214 | Adu79214 Human pep |
| 356 | 27 | 28.7 | 21 | 8 | ADK15980 | Adk15980 Human pro |
| 357 | 27 | 28.7 | 22 | 2 | AAR48765 | Aar48765 G-protein |
| 358 | 27 | 28.7 | 22 | 2 | AAW02737 | Aaw02737 G-protein |
| 359 | 27 | 28.7 | 22 | 2 | AAY27485 | Aay27485 E. coli b |
| 360 | 27 | 28.7 | 22 | 4 | AAM15199 | Aam15199 Peptide # |
| 361 | 27 | 28.7 | 22 | 4 | AAM27656 | Aam27656 Peptide # |
| 362 | 27 | 28.7 | 22 | 4 | AAM67366 | Aam67366 Human bon |

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| 363 | 27 | 28.7 | 22 | 4 | AAM02939 | Aam02939 Peptide # |
| 364 | 27 | 28.7 | 22 | 5 | AAM49327 | Aam49327 HIV-1 gp1 |
| 365 | 27 | 28.7 | 23 | 5 | AAU86417 | Aau86417 Androgen |
| 366 | 27 | 28.7 | 24 | 8 | ADY81099 | Ady81099 Rice leaf |
| 367 | 27 | 28.7 | 24 | 9 | ADV25923 | Adv25923 SARS coro |
| 368 | 27 | 28.7 | 25 | 2 | AAY33334 | Aay33334 P. monodo |
| 369 | 27 | 28.7 | 25 | 3 | AAB22956 | Aab22956 Tiger pra |
| 370 | 27 | 28.7 | 25 | 3 | AAY93925 | Aay93925 N-termina |
| 371 | 27 | 28.7 | 25 | 4 | AAE07931 | Aae07931 N-termina |
| 372 | 27 | 28.7 | 25 | 5 | AAO21348 | Aao21348 Panaeus m |
| 373 | 27 | 28.7 | 25 | 6 | ABP99568 | Abp99568 Human sec |
| 374 | 27 | 28.7 | 25 | 9 | ADY81712 | Ady81712 Krill-der |
| 375 | 27 | 28.7 | 25 | 10 | AEE39235 | Aee39235 Human ser |
| 376 | 27 | 28.7 | 26 | 2 | AAW01183 | Aaw01183 Serine pr |
| 377 | 27 | 28.7 | 26 | 3 | AAB39185 | Aab39185 Human sec |
| 378 | 27 | 28.7 | 26 | 4 | AAB50579 | Aab50579 Flea seri |
| 379 | 27 | 28.7 | 27 | 2 | AAR25352 | Aar25352 Calcitoni |
| 380 | 27 | 28.7 | 27 | 4 | ABB36341 | Abb36341 Peptide # |
| 381 | 27 | 28.7 | 27 | 4 | ABB31146 | Abb31146 Peptide # |
| 382 | 27 | 28.7 | 27 | 5 | ABG39127 | Abg39127 Human pep |
| 383 | 27 | 28.7 | 27 | 7 | ADK14963 | Adk14963 Urinary s |
| 384 | 27 | 28.7 | 27 | 7 | ADL66715 | Adl66715 Shg prote |
| 385 | 27 | 28.7 | 27 | 8 | ABO60614 | Abo60614 Human gen |
| 386 | 27 | 28.7 | 28 | 3 | AAB22001 | Aab22001 Human V g |
| 387 | 27 | 28.7 | 28 | 5 | AAE23914 | Aae23914 Human TCR |
| 388 | 27 | 28.7 | 28 | 10 | AEE28088 | Aee28088 N. mening |
| 389 | 27 | 28.7 | 29 | 2 | AAR30298 | Aar30298 [Nva 0,Le |
| 390 | 27 | 28.7 | 29 | 2 | AAR30286 | Aar30286 [Val 0,Le |
| 391 | 27 | 28.7 | 29 | 2 | AAR30333 | Aar30333 [Ala 0, L |
| 392 | 27 | 28.7 | 29 | 2 | AAR30292 | Aar30292 [Thr 0,Le |
| 393 | 27 | 28.7 | 29 | 2 | AAR30325 | Aar30325 [Ile 0, L |
| 394 | 27 | 28.7 | 29 | 2 | AAR30329 | Aar30329 [Thr 0, L |
| 395 | 27 | 28.7 | 29 | 2 | AAR30335 | Aar30335 [Nva 0, L |
| 396 | 27 | 28.7 | 29 | 2 | AAR30296 | Aar30296 [Ala 0,Le |
| 397 | 27 | 28.7 | 29 | 2 | AAR30323 | Aar30323 [Val 0, L |
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| 399 | 27 | 28.7 | 29 | 2 | AAR30331 | Aar30331 [Ser 0, L |
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| 402 | 27 | 28.7 | 29 | 2 | AAR30294 | Aar30294 [Ser 0,Le |
| 403 | 27 | 28.7 | 29 | 2 | AAR30321 | Aar30321 [Leu 0,8, |
| 404 | 27 | 28.7 | 29 | 2 | AAR30327 | Aar30327 [Met 0, L |
| 405 | 27 | 28.7 | 29 | 2 | AAR30288 | Aar30288 [Ile 0,Le |
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| 407 | 27 | 28.7 | 29 | 4 | AAU27336 | Aau27336 Novel bon |
| 408 | 27 | 28.7 | 29 | 5 | AAE13588 | Aae13588 Glutathio |
| 409 | 27 | 28.7 | 29 | 8 | ADT41179 | Adt41179 hSARS vir |
| 410 | 27 | 28.7 | 29 | 8 | ADS80594 | Ads80594 SARS viru |
| 411 | 27 | 28.7 | 29 | 8 | ADT38709 | Adt38709 hSARS vir |
| 412 | 27 | 28.7 | 29 | 8 | ADU99091 | Adu99091 Human 109 |
| 413 | 27 | 28.7 | 29 | 8 | ADU99088 | Adu99088 Human 109 |
| 414 | 27 | 28.7 | 29 | 9 | AEB27671 | Aeb27671 pGEX-KG v |
| 415 | 27 | 28.7 | 29 | 9 | AEC65508 | Aec65508 Human 109 |
| 416 | 27 | 28.7 | 29 | 9 | AEC65505 | Aec65505 Human 109 |
| 417 | 27 | 28.7 | 30 | 8 | ADX95629 | Adx95629 Plant ful |
| 418 | 27 | 28.7 | 30 | 9 | AEE68223 | Aee68223 Cottontai |
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| 420 | 26.5 | 28.2 | 22 | 9 | AEE22843 | Aee22843 Human IL- |
| 421 | 26.5 | 28.2 | 24 | 10 | AEE37361 | Aee37361 Human ser |
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|---|---|---|---|---|---|---|
| 424 | 26 | 27.7 | 9 | 4 | AAE09516 | Aae09516 Human muc |
| 425 | 26 | 27.7 | 9 | 4 | AAE09517 | Aae09517 Human muc |
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| 428 | 26 | 27.7 | 9 | 7 | ADE69119 | Ade69119 Human 161 |
| 429 | 26 | 27.7 | 9 | 7 | ADE78017 | Ade78017 Synthetic |
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| 432 | 26 | 27.7 | 10 | 6 | ABR19695 | Abr19695 Human can |
| 433 | 26 | 27.7 | 10 | 6 | ABR19958 | Abr19958 Human can |
| 434 | 26 | 27.7 | 10 | 6 | ABR19296 | Abr19296 Human can |
| 435 | 26 | 27.7 | 10 | 6 | ABR18879 | Abr18879 Human can |
| 436 | 26 | 27.7 | 10 | 6 | ABJ67340 | Abj67340 184P1E2-r |
| 437 | 26 | 27.7 | 10 | 6 | ABJ66616 | Abj66616 184P1E2-r |
| 438 | 26 | 27.7 | 10 | 6 | ABJ65906 | Abj65906 184P1E2-r |
| 439 | 26 | 27.7 | 10 | 6 | ABJ69262 | Abj69262 184P1E2-r |
| 440 | 26 | 27.7 | 10 | 6 | ABJ68663 | Abj68663 184P1E2-r |
| 441 | 26 | 27.7 | 10 | 6 | ABJ67896 | Abj67896 184P1E2-r |
| 442 | 26 | 27.7 | 10 | 6 | AAE38125 | Aae38125 Human cyt |
| 443 | 26 | 27.7 | 10 | 7 | ADE69291 | Ade69291 Human 161 |
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| 446 | 26 | 27.7 | 10 | 7 | ADE66364 | Ade66364 Human 161 |
| 447 | 26 | 27.7 | 10 | 7 | ADW33062 | Adw33062 HLA bindi |
| 448 | 26 | 27.7 | 11 | 2 | AAR32183 | Aar32183 Ranakinin |
| 449 | 26 | 27.7 | 11 | 5 | ABG67301 | Abg67301 Human ADP |
| 450 | 26 | 27.7 | 11 | 6 | ABP74753 | Abp74753 Proteome |
| 451 | 26 | 27.7 | 11 | 6 | ABR75650 | Abr75650 Liver res |
| 452 | 26 | 27.7 | 11 | 6 | ADA23401 | Ada23401 Alzheimer |
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| 454 | 26 | 27.7 | 13 | 2 | AAW37160 | Aaw37160 Human TcA |
| 455 | 26 | 27.7 | 13 | 7 | ADD43994 | Add43994 CPG2 pept |
| 456 | 26 | 27.7 | 13 | 10 | AEE30765 | Aee30765 Represent |
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| 458 | 26 | 27.7 | 14 | 1 | AAP91703 | Aap91703 Human tum |
| 459 | 26 | 27.7 | 14 | 2 | AAR57740 | Aar57740 Human tum |
| 460 | 26 | 27.7 | 14 | 5 | AAB71445 | Aab71445 Human C3 |
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| 462 | 26 | | | | | |

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AC   AAW54070;
XX
DT   10-AUG-1998  (first entry)
XX
DE   IVI-4 protein fragment of E. faecalis.
XX
KW   IVI-2 locus; ivi-3 protein; ivi-4 protein; transcriptional regulator;
KW   antibiotic testing; infection; endocarditis; therapy.
XX
OS   Enterococcus faecalis.
XX
PN   WO9812205-A1.
XX
PD   26-MAR-1998.
XX
PF   18-SEP-1997;   97WO-US016589.
XX
PR   18-SEP-1996;   96US-0025899P.
XX
PA   (VIRU-) VIRUS RES INST INC.
XX
PI   Beattie DT;
XX
DR   WPI; 1998-217198/19.
DR   N-PSDB; AAV24034.
XX
PT   Enterococcus faecalis transcriptional regulators ivi-2 and ivi-3, and ivi
PT   -4 - useful to test antibiotics, to identify pharmaceuticals for treating
PT   or controlling E. faecalis infections, particularly endocarditis.
XX
PS   Claim 1; Fig 1; 36pp; English.
XX
CC   This sequence is a ivi-4 fragment from Enterococcus faecalis. It is
CC   encoded by the DNA sequence of the invention, which encodes the mature
CC   ivi-2, and ivi-3 proteins, and also contains a partial ivi-4 protein
CC   coding sequence. Ivi-2 and ivi-3 are Enterococcus faecalis
CC   transcriptional regulator ivi-2 or ivi-3. Ivi-2 and ivi-3 can be used as
CC   reagents for testing antibiotics for their activity in deactivating or
CC   controlling their activity as part of a screening process to identify
CC   pharmaceuticals for treating or controlling E. faecalis infections,
CC   particularly endocarditis. The DNA sequence can be used in the generation
CC   of antisense oligonucleotides or probes for the treatment and
CC   identification of E. faecalis infection. The products are also useful as
CC   in vitro agents for producing monoclonal antibodies, useful in diagnostic
CC   and screening procedures for identifying or treating E. faecalis
CC   infections
XX
SQ   Sequence 28 AA;

  Query Match             35.1%;  Score 33;  DB 2;  Length 28;
  Best Local Similarity   62.5%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 LELMPNIE 17
               ||:|||::
Db          12 LEIMPNVK 19
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Q8L2T5_NEIME
ID   Q8L2T5_NEIME   PRELIMINARY;   PRT;    18 AA.
AC   Q8L2T5;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Tryptophan transporter (Fragment).
OS   Neisseria meningitidis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Neisseria.
OX   NCBI_TaxID=487;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=126E;
RX   MEDLINE=22051050; PubMed=12055303;
RA   Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;
RT   "Genetic diversity of three lgt loci for biosynthesis of
RT   lipooligosaccharide (LOS) in Neisseria species.";
RL   Microbiology 148:1833-1844(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF470685; AAM33537.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   18 AA;  1944 MW;  08DE06F3E9B8C27E CRC64;

  Query Match             41.5%;  Score 39;  DB 2;  Length 18;
  Best Local Similarity   35.7%;  Pred. No. 82;
  Matches    5;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 NLSSDIIGQLELMP 14
              |::: :: |:||:|
Db          1 NIAAQVLSQMELVP 14
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```
 Sequence 530, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
;  APPLICANT: EDWARDS, ALED
;  APPLICANT:  DHARAMSI, AKIL
;  APPLICANT:  VEDADI, MASOUD
;  TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
;  FILE REFERENCE: IPT-330.01
;  CURRENT APPLICATION NUMBER: US/11/122,986
;  CURRENT FILING DATE:  2005-05-05
;  PRIOR APPLICATION NUMBER: 60/423,875
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,832
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,915
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,757
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,758
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/424,367
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,376
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,370
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,362
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,373
;  PRIOR FILING DATE: 2002-11-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 844
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 530
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-11-122-986-530

  Query Match             27.7%;  Score 26;  DB 7;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 NIERF 19
              |||||
Db          1 NIERF 5
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 Sequence 41, Application US/10147140
; Publication No. US20030153730A1
; GENERAL INFORMATION:
;  APPLICANT: STRACKE, MARY
;  APPLICANT:  LIOTTA, LANCE
;  APPLICANT:  SCHIFFMANN, ELLIOTT
;  APPLICANT:  KRUTZCH, HENRY
;  APPLICANT:  MURATA, JUN
;  TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
;  TITLE OF INVENTION:  CANCER DIAGNOSIS AND THERAPY
;  FILE REFERENCE: 2026-4149US4
;  CURRENT APPLICATION NUMBER: US/10/147,140
;  CURRENT FILING DATE:  2002-05-15
;  PRIOR APPLICATION NUMBER: 07/822,043
;  PRIOR FILING DATE: 1992-01-17
;  PRIOR APPLICATION NUMBER: 08/249,182
;  PRIOR FILING DATE: 1994-05-25
;  PRIOR APPLICATION NUMBER: 08/346,455
;  PRIOR FILING DATE: 1994-11-28
;  PRIOR APPLICATION NUMBER: 08/977,221
;  PRIOR FILING DATE: 1997-11-24
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-147-140-41

  Query Match             31.9%;  Score 30;  DB 4;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+06;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 LMPNIER 18
              :|||||:
Db          1 VMPNIEK 7
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```
 Sequence 40, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
;  APPLICANT: ROSENZWEIG, Michael
;  APPLICANT:  PYKETT, Mark J.
;  APPLICANT:  SCADDEN, David T.
;  APPLICANT:  POZNANSKY, Mark C.
;  TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
;  TITLE OF INVENTION:  FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
;  TITLE OF INVENTION:  DEVICES
;  FILE REFERENCE: C1005/7012/KA/ERG
;  CURRENT APPLICATION NUMBER: US/10/161,097
;  CURRENT FILING DATE:  2002-05-31
;  PRIOR APPLICATION NUMBER: US/09/574,749
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: US 60/107,972
;  PRIOR FILING DATE: 1998-11-12
;  PRIOR APPLICATION NUMBER: PCT/US99/26795
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: US 09/524,749
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Measles source
US-10-161-097-40

  Query Match             30.9%;  Score 29;  DB 4;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 9e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 LELMPNI 16
              ::|||||
Db          6 IKLMPNI 12
```

```
 Sequence 7, Application US/09147857
; Patent No. 6376235
; GENERAL INFORMATION:
;  APPLICANT:  Beattie, David T.
;  TITLE OF INVENTION:  IVI-2, IVI-3 and IVI-4 Loci of Enterococcus Faecalis
;  TITLE OF INVENTION:  Polynucleotide, Polypeptides and Method of Use Therefor
;  FILE REFERENCE:  732250-215
;  CURRENT APPLICATION NUMBER: US/09/147,857
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER:  U.S. 60/025,899
;  PRIOR FILING DATE:  1996-09-18
;  PRIOR APPLICATION NUMBER:  PCT/US97/16589
;  PRIOR FILING DATE:  1997-09-18
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Deduced amino
;   OTHER INFORMATION: acid sequence of a portion of IVI-4 polypeptide
US-09-147-857-7

  Query Match             35.1%;  Score 33;  DB 2;  Length 28;
  Best Local Similarity   62.5%;  Pred. No. 82;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 LELMPNIE 17
               ||:|||:: 
Db          12 LEIMPNVK 19
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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_519_537
Perfect score: 94
Sequence: 1 NLSSDIIGQLELMPNIERF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 94 | 100.0 | 19 | 9 | ADW11046 | Adw11046 Clostridi |
| 2 | 94 | 100.0 | 27 | 9 | ADW11104 | Adw11104 Clostridi |
| 3 | 47 | 50.0 | 27 | 9 | ADW11105 | Adw11105 Clostridi |
| 4 | 38 | 40.4 | 24 | 2 | AAR84289 | Aar84289 Aq. elcat |
| 5 | 37 | 39.4 | 30 | 2 | AAR07952 | Aar07952 Synthetic |

```
 Sequence 40, Application US/09574749B
; Patent No. 6548299
; GENERAL INFORMATION:
;  APPLICANT: ROSENZWEIG, Michael
;  APPLICANT:  PYKETT, Mark J.
;  APPLICANT:  SCADDEN, David T.
;  APPLICANT:  POZNANSKY, Mark C.
;  TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
;  TITLE OF INVENTION:  FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
;  TITLE OF INVENTION:  DEVICES
;  FILE REFERENCE: C1005/7012/KA/ERG
;  CURRENT APPLICATION NUMBER: US/09/574,749B
;  CURRENT FILING DATE:  2002-05-31
;  PRIOR APPLICATION NUMBER: US 60/107,972
;  PRIOR FILING DATE: 1998-11-12
;  PRIOR APPLICATION NUMBER: PCT/US99/26795
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: US 09/524,749
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Measles source
US-09-574-749B-40

  Query Match           30.9%;  Score 29;  DB 2;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 LELMPNI 16
              ::|||||
Db          6 IKLMPNI 12
```

```
Sequence 44, Application US/08433522A
; Patent No. 6013514
;  GENERAL INFORMATION:
;    APPLICANT:  CHONG, Pele
;    APPLICANT:  THOMAS, Wayne
;    APPLICANT:  YANG, Yan Ping
;    APPLICANT:  LOOSMORE, Sheena
;    APPLICANT:  SIA, Dwo Yuan Charles
;    APPLICANT:  KLEIN, Michel
;    TITLE OF INVENTION:  HAEMOPHILUS OUTER MEMBRANE PROTEIN
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6TH Floor, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/433,522A
;      FILING DATE:  12-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEWART, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-434 MIS:jb
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-433-522A-44

  Query Match             30.9%;  Score 29;  DB 2;  Length 27;
  Best Local Similarity   71.4%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LSSDIIG 8
              :|||:||
Db         21 ISSDVIG 27
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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:30:50 ; Search time 99.3 Seconds
(without alignments)
176.992 Million cell updates/sec

Title: US-10-821-669-1_COPY_533_551
Perfect score: 105
Sequence: 1 NIERFPNGKKYELDKYTMF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 36 | 34.3 | 19 | 2 | Q4Z5V1_PLABE | Q4z5v1 plasmodium |
| 2 | 34.5 | 32.9 | 26 | 2 | Q4YE51_PLABE | Q4ye51 plasmodium |
| 3 | 33 | 31.4 | 23 | 2 | Q4XN62_PLACH | Q4xn62 plasmodium |

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RESULT 19
US-10-334-726-299
; Sequence 299, Application US/10334726
; Publication No. US20030211521A1
; GENERAL INFORMATION:
;  APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
;  TITLE OF INVENTION: BREAST CANCER ANTIGEN
;  FILE REFERENCE: 1090-36
;  CURRENT APPLICATION NUMBER: US/10/334,726
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: US/09/645,446
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: PCT/GB99/00866
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: GB 9805877.9
;  PRIOR FILING DATE: 1998-09-20
;  NUMBER OF SEQ ID NOS: 324
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 299
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:predicted
;   OTHER INFORMATION: peptide
US-10-334-726-299

  Query Match             30.5%;  Score 32;  DB 4;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+06;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ERFPNGKK 10
              |  |||||
Db          1 EPLPNGKK 8
```

```
Sequence 8, Application US/09925442
; Patent No. US20020103346A1
;   GENERAL INFORMATION:
;        APPLICANT: VOGEL, CARL-WILHELM
;                   BREDEHORST, REINHORST
;                   KOCK, MICHAEL
;                   FRITZINGER, DAVID
;        TITLE OF INVENTION: RECOMBINANT PROCVF
;        NUMBER OF SEQUENCES: 39
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;                        P.C.
;             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22202
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/925,442
;             FILING DATE: 10-Aug-2001
;             CLASSIFICATION:
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/017,947
;             FILING DATE:
;        ATTORNEY/AGENT INFORMATION:
;             NAME: OBLON, NORMAN F.
;             REGISTRATION NUMBER: 24,618
;             REFERENCE/DOCKET NUMBER: 1126-0107-0X
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-413-3000
;             TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-925-442-8
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533-551

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  Query Match             30.5%;  Score 32;  DB 3;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 KYELDK 15
              ||||||
Db          7 KYELDK 12
```

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Sequence 51, Application US/08447411
; Patent No. 5773243
;  GENERAL INFORMATION:
;    APPLICANT:  FRITZINGER, DAVID C.
;    APPLICANT:  BREDEHORST, REINHARD
;    APPLICANT:  VOGEL, CARL-WILHELM
;    TITLE OF INVENTION:  DNA ENCODING COBRA C3, CVF1, AND CVF2
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,411
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/043,747
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5773243man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-101-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-447-411-51

  Query Match             30.5%;  Score 32;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 KYELDK 15
              ||||||
Db          7 KYELDK 12
```

```
Sequence 8, Application US/08662227
; Patent No. 5922320
;  GENERAL INFORMATION:
;    APPLICANT:  VOGEL, CARL-WILHELM
;    APPLICANT:  BREDEHORST, REINHORST
;    APPLICANT:  KOCK, MICHAEL
;    APPLICANT:  FRITZINGER, DAVID
;    TITLE OF INVENTION:  RECOMBINANT PROCVF
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/662,227
;      FILING DATE:  14-JUN-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-0107-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-662-227-8

  Query Match          30.5%;  Score 32;  DB 1;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 KYELDK 15
              ||||||
Db          7 KYELDK 12
```

OS Hepatitis C virus.
OS Synthetic.
XX
PN WO2004069864-A1.
XX
PD 19-AUG-2004.
XX
PF 29-DEC-2003; 2003WO-FR003922.
XX
PR 07-JAN-2003; 2003FR-00000094.
XX
PA (INMR ) BIOMERIEUX SA.
PA (CNRS ) CENT NAT RECH SCI.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
XX
PI Bain C, Inchauspe G, Lavergne J, Parroche P, Penin F;
XX
DR WPI; 2004-625448/60.
XX
PT New immunogenic polypeptide form hepatitis C virus, useful for treatment,
PT prevention and diagnosis of infection, also related epitopes, nucleic
PT acids and antibodies.
XX
PS Claim 12; SEQ ID NO 298; 231pp; French.
XX
CC The present invention describes polypeptide F' (I) that induces an immune
CC response against the hepatitis C virus (HCV) and comprises the 99 amino
CC acids (aa) present between positions 43 and 141 of the HCV polyprotein.
CC Also described: (1) nucleic acid sequences (II) that encode (I); (2) an
CC epitope (E) that induces a response against HCV and comprises the 9 aa
CC between positions 40 and 48, 43 and 51, 50 and 58 or 73 and 81 of the HCV
CC polyprotein; (3) nucleic acid sequences (IIa) that encode (E); (4) an
CC expression vector that contains (II) or (IIa), or two (IIa), and
CC necessary expression elements; (5) microorganisms or host cells
CC transformed by at least one vector of (4); (6) antibodies (Ab) directed
CC against (I) or (E); and (7) a method for the detection and/or
CC quantification of HCV using Ab. (I) has virucide, hepatotropic and
CC antiinflammatory activities, and can be used in vaccines. (I) induces a
CC cell-mediated response in subjects seropositive for HCV and particularly
CC secretion of interleukin-10, optionally also of interferon-gamma. They
CC are effective in patients infected with viral genotypes 1b and 3,
CC whatever their HLA type. (I) and their epitopes can be used to inhibit,
CC prevent or treat hepatitis C virus infection in animals, especially
CC humans, particularly as vaccines, and including where nucleic acid
CC sequences (II), or vectors containing them, are used to express (I) or
CC (E). The method can particularly be used in subjects who do not respond
CC well to treatment with interferon and ribavirine. (I), (II) and
CC antibodies directed against (I) or (E), can be used for diagnostic
CC determination and/or quantification of HCV, in vitro. The present
CC sequence represents an anti-HCV immunogenic protein F' epitope peptide,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 30.5%; Score 32; DB 8; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 RFPNGKK 10
              |||:|:|
Db          1 RFPSGRK 7
```

RESULT 46
ADZ75857
ID ADZ75857 standard; peptide; 21 AA.
XX
AC ADZ75857;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human non-selenium glutathione peroxidase (NSGP) antigenic peptide SEQ:2.
XX
KW Diagnosis; oxidative stress; neurodegenerative disease;
KW neurological disease; Alzheimers disease; Parkinsons disease; dementia;
KW non-selenium glutathione peroxidase; Ca2+-independent phospholipase A2;
KW antigen.
XX
OS Homo sapiens.
XX
PN US2005100979-A1.
XX
PD 12-MAY-2005.
XX
PF 29-AUG-2003; 2003US-00651056.
XX
PR 30-SEP-2002; 2002AU-00951775.
XX
PA (POWE/) POWER J H T.
XX
PI Power JHT;
XX
DR WPI; 2005-365635/37.
XX
PT Diagnosing a disease state associated with oxidative stress, for
PT detecting or treating neurodegenerative disease, comprises measuring the
PT level of non-selenium glutathione peroxidase protein in a biological
PT fluid or tissue.
XX
PS Claim 14; SEQ ID NO 2; 17pp; English.
XX
CC The invention relates to a method of diagnosing a disease state
CC associated with oxidative stress by measuring the level of non-selenium
CC glutathione peroxidase (NSGP, also known as lysosomal type Ca2+-
CC independent phospholipase A2) protein in a biological fluid or tissue
CC obtained from a patient. The level of NSGP protein may be compared to a
CC control, or may be measured in samples taken from the patient over a
CC period of time, and is preferably determined using an NSGP-specific
CC antibody. An increase in the level of NSGP protein measured is indicative
CC of neuronal oxidative stress, which has been implicated as a cause of
CC neurodegenerative diseases such as Alzheimer's disease, Parkinson's
CC disease and dementia. The invention also relates to NSGP-specific
CC antibodies raised against one of two specific NSGP peptide fragments
CC (ADZ75856-ADZ75857, and a method of detecting oxidative stress in an
CC individual using NSGP-specific antibodies. The invention further
CC discloses methods for producing NSGP-specific antibodies, an immunogenic
CC composition comprising the NSGP peptide fragments ADZ75856-ADZ75857, and
CC a method for inhibiting or alleviating one or more symptoms of a
CC neurodegenerative disease using a substance that upregulates NSGP
CC expression or mimics its activity. The methods of the invention are
CC useful for the diagnosis of oxidative stress or a disease related to
CC oxidative stress, especially Alzheimer's disease, Parkinson's disease and
CC dementia. The present sequence represents a specifically claimed C-

CC terminal antigenic peptide fragment of human NSGP (corresponding to
CC residues 199-219 of NSGP, ADZ75858) that is recognized by antibodies of
CC the invention.
XX
SQ Sequence 21 AA;

Query Match 30.5%; Score 32; DB 9; Length 21;
Best Local Similarity 55.6%; Pred. No. 7.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 ERFPNGKKY 11
              :  |:||||
Db         11 KELPSGKKY 19
```

GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_547_565
Perfect score: 105
Sequence: 1 KYTMFHYLRAQEFEHGKSR 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 105 | 100.0 | 19 | 9 | ADW11048 | Adw11048 Clostridi |
| 2 | 105 | 100.0 | 27 | 9 | ADW11106 | Adw11106 Clostridi |
| 3 | 52 | 49.5 | 27 | 9 | ADW11105 | Adw11105 Clostridi |
| 4 | 49 | 46.7 | 27 | 9 | ADW11107 | Adw11107 Clostridi |
| 5 | 47 | 44.8 | 8 | 9 | ADZ69794 | Adz69794 Botulinum |
| 6 | 43 | 41.0 | 13 | 5 | ABG97927 | Abg97927 Human INF |

```
ADH78637
ID   ADH78637 standard; peptide; 15 AA.
XX
AC   ADH78637;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human fibroblast interferon-beta protein based peptide, SEQ ID No 45.
XX
KW   T-cell epitope; cytokine; receptor; CD4+; CD8+; immunogenicity;
KW   interferon-beta; tumour necrosis factor receptor-1; erythropoietin;
KW   thrombopoietin; inflammation; cancer; anaemia;
KW   human fibroblast interferon-beta.
XX
OS   Homo sapiens.
XX
PN   WO2003104263-A2.
XX
PD   18-DEC-2003.
XX
PF   26-FEB-2003; 2003WO-US005917.
XX
PR   01-MAY-2002; 2002US-0376743P.
XX
PA   (GEMV ) GENENCOR INT INC.
XX
PI   Harding FA,  Power SD;
XX
DR   WPI; 2004-062306/06.
XX
PT   Determining T-cell epitope of a protein (e.g. cytokine or cytokine
PT   receptor), useful for reducing protein allergenicity, comprises combining
PT   differentiated dendritic cells and naive T-cells with a peptide having
PT   the T-cell epitope.
XX
PS   Example 2; SEQ ID NO 45; 51pp; English.
XX
CC   The invention relates to a novel method for determining a T-cell epitope
CC   of a protein, where the protein is selected from cytokines and cytokine
CC   receptors. The method comprises combining a solution of differentiated
CC   dendritic cells and naive CD4+ and/or CD8+ T-cells with a pepset of
CC   peptides comprising the T-cell epitope. The composition and methods are
CC   useful in reducing the immunogenicity of cytokines and cytokine receptors
CC   such as interferon-beta, soluble tumour necrosis factor receptor-1,
CC   erythropoietin or thrombopoietin. These modified cytokines and cytokine
CC   receptors may be used for treating various conditions such as
CC   inflammation, cancer or anaemia. This sequence represents a peptide based
CC   on the human fibroblast interferon-beta protein sequence of the
CC   invention.
XX
SQ   Sequence 15 AA;

  Query Match             32.4%;  Score 34;  DB 8;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 97;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQEF 13
              |||:|:|:
Db          2 HYLKAKEY 9
```

```
Q08578_HUMAN
ID   Q08578_HUMAN   PRELIMINARY;   PRT;    27 AA.
AC   Q08578;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Complement receptor (Fragment).
GN   Name=CR2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93018869; PubMed=1383386; DOI=10.1084/jem.176.5.1405;
RA   Birkenbach M., Tong X., Brandbury L.E., Tedder T.F., Kieff E.;
RT   "Characterization of a epstein-bar virus receptor on human epithelial
RT   cells.";
RL   J. Exp. Med. 176:1405-1414(1992).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; X68990; CAA48779.1; -; mRNA.
DR   PIR; I37261; I37261.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER      27     27
SQ   SEQUENCE   27 AA;  2912 MW;  8A12201A98A6DA60 CRC64;

  Query Match             27.6%;  Score 29;  DB 2;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQ 11
              |||||:
Db          9 HYLRAR 14
```

```
Sequence 5, Application US/09029052A
; Patent No. 6140043
; GENERAL INFORMATION:
;  APPLICANT: Dierich, Manfred P
;  APPLICANT: Chen, Ying Hua
;  TITLE OF INVENTION: Pharmaceutical compositions for competitively
;  TITLE OF INVENTION: inhibiting the binding of a retrovirus to the
;  TITLE OF INVENTION: IFN-receptor and means for diagnosis of an HIV
;  TITLE OF INVENTION: infection.
;  FILE REFERENCE: 147-169P
;  CURRENT APPLICATION NUMBER: US/09/029,052A
;  CURRENT FILING DATE: 1998-04-20
;  EARLIER APPLICATION NUMBER: PCT/EP96/03648
;  EARLIER FILING DATE: 1995-08-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Source of Artificial Sequence: synthesized from
;   OTHER INFORMATION: the human IFN-beta receptor binding region 2
;   OTHER INFORMATION: (aa123-140)
US-09-029-052-5

  Query Match             41.0%;  Score 43;  DB 2;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 0.55;
  Matches    6;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MFHYLRAQEFEH 15
              : |||:|:|: |
Db          5 ILHYLKAKEYSH 16
```

```
Sequence 103, Application US/10038612
; Patent No. 6723830
; GENERAL INFORMATION:
;  APPLICANT: Ben-Sasson, Shmuel A.
;  TITLE OF INVENTION: Short Peptides Which Selectively
;  TITLE OF INVENTION:  Modulate the Activity of Protein Kinases
;  FILE REFERENCE: 1242.1029-000 (CMCC-679)
;  CURRENT APPLICATION NUMBER: US/10/038,612
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US 09/161,094
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: MYRISTATE
;   LOCATION: (1)...(0)
;   NAME/KEY: AMIDATION
;   LOCATION: (0)...(21)
;   OTHER INFORMATION: c-Sea
US-10-038-612-103

  Query Match             30.5%;  Score 32;  DB 2;  Length 21;
  Best Local Similarity   71.4%;  Pred. No. 61;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQE 12
              |::||||
Db         12 HFIRAQE 18
```

```
Sequence 113, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
;  GENERAL INFORMATION:
;    APPLICANT:  Dower, William J.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Cwirla, Steven E.
;    APPLICANT:  Gates, Christian
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Balasubramanian, Palaniappan
;    APPLICANT:  Wagstrom, Christopher R.
;    APPLICANT:  Hendren, Richard W.
;    APPLICANT:  Deprince, Randolph B.
;    APPLICANT:  Podduturi, Surekha
;    APPLICANT:  Yin, Qun
;    TITLE OF INVENTION:  PEPTIDES AND COMPOUNDS THAT BIND TO A
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  244
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Glaxo Wellcome
;      STREET:  Five Moore Drive, P.O. Box 13398
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,640
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hrubiec, Robert T.
;      REGISTRATION NUMBER:  36,392
;      REFERENCE/DOCKET NUMBER:  PK3281
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-248-1000
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-764-640-113

  Query Match             29.5%;  Score 31;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 39;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 QEFEHG 16
               |||:||
Db           4 QEFKHG 9
```

```
 Sequence 113, Application US/09244298A
; Patent No. 6121238
;  GENERAL INFORMATION:
;    APPLICANT:  Dower, William J.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Cwirla, Steven E.
;    APPLICANT:  Gates, Christian
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Balasubramanian, Palaniappan
;    APPLICANT:  Wagstrom, Christopher R.
;    APPLICANT:  Hendren, Richard W.
;    APPLICANT:  Deprince, Randolph B.
;    APPLICANT:  Podduturi, Surekha
;    APPLICANT:  Yin, Qun
;    TITLE OF INVENTION:  PEPTIDES AND COMPOUNDS THAT BIND TO A
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  244
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Glaxo Wellcome
;      STREET:  Five Moore Drive, P.O. Box 13398
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/244,298A
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hrubiec, Robert T.
;      REGISTRATION NUMBER:  36,392
;      REFERENCE/DOCKET NUMBER:  PK3281
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-248-1000
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-244-298A-113

  Query Match             29.5%;  Score 31;  DB 2;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 39;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 QEFEHG 16
              |||:||
Db          4 QEFKHG 9
```

```
Sequence 69, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 548-555)
US-10-715-810-69

  Query Match             44.8%;  Score 47;  DB 5;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YTMFHYLR 9
              ||||||||
Db          1 YTMFHYLR 8
```

```
Sequence 76, Application US/10471894B
; Publication No. US20050054052A1
; GENERAL INFORMATION:
;  APPLICANT: Carr, Francis J.
;  APPLICANT:  Carter, Graham
;  APPLICANT:  Jones, Tim
;  APPLICANT:  Watkins, John
;  APPLICANT:  Baker, Matthew
;  TITLE OF INVENTION: MODIFIED INTERFERON BETA WITH REDUCED
;  TITLE OF INVENTION:  IMMUNOGENICITY
;  FILE REFERENCE: MER-124
;  CURRENT APPLICATION NUMBER: US/10/471,894B
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/EP02/02925
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: EP 01106539.8
;  PRIOR FILING DATE: 2001-03-15
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MHC class II binding epitope
US-10-471-894B-76

  Query Match             40.0%;  Score 42;  DB 5;  Length 13;
  Best Local Similarity   60.0%;  Pred. No. 8.6;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 HYLRAQEFEH 15
              |||:|:|: |
Db          1 HYLKAKEYSH 10
```

```
Sequence 141, Application US/10820467
; Publication No. US20050054053A1
; GENERAL INFORMATION:
;  APPLICANT: Aguinaldo, Anna Marie
;  APPLICANT:  Beyna, Amelia Joy
;  APPLICANT:  Cho, Ho Sung
;  APPLICANT:  Desjarlais, John Rudolph
;  APPLICANT:  Marshall, Shannon Alicia
;  APPLICANT:  Muchhal, Umesh
;  APPLICANT:  Villegas, Michael Francis Aquino
;  APPLICANT:  Zhukovsky, Eugene
;  APPLICANT:  Quesenberry, Michael Stephen
;  TITLE OF INVENTION: INTERFERON VARIANTS WITH IMIPROVED PROPERTIES
;  FILE REFERENCE: A-71431-4
;  CURRENT APPLICATION NUMBER: US/10/820,467
;  CURRENT FILING DATE:  2004-03-30
;  PRIOR APPLICATION NUMBER: US 60/477,246
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: US 60/415,541
;  PRIOR FILING DATE: 2002-10-01
;  PRIOR APPLICATION NUMBER: US 60/489,725
;  PRIOR FILING DATE: 2003-07-24
;  PRIOR APPLICATION NUMBER: US 10/676,705
;  PRIOR FILING DATE: 2003-09-30
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-820-467-141

  Query Match             32.4%;  Score 34;  DB 5;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+06;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQEF 13
              |||:|:|:
Db          2 HYLKAKEY 9


RESULT 21
```

```
Sequence 61, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
;  APPLICANT: Ben-Sasson, Shmuel A.
;  TITLE OF INVENTION: Short Peptides Which Selectively
;  TITLE OF INVENTION:  Modulate the Activity of Protein Kinases
;  FILE REFERENCE: 1242.1029-000 (CMCC-679)
;  CURRENT APPLICATION NUMBER: US/10/038,612
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US 09/161,094
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: unknown
;   FEATURE:
;   OTHER INFORMATION: c-Sea
US-10-038-612-61

  Query Match             30.5%;  Score 32;  DB 4;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 5.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQE 12
              |::||||
Db         11 HFIRAQE 17
```

```
Sequence 198, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
;  CURRENT APPLICATION NUMBER: US/09/755,630A
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 293
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-198

  Query Match             28.6%;  Score 30;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

```
Sequence 198, Application US/10658180
; Publication No. US20040216187A1
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.DVUS02
;  CURRENT APPLICATION NUMBER: US/10/658,180
;  CURRENT FILING DATE:  2003-09-09
;  PRIOR APPLICATION NUMBER: US 09/755,630
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-10-658-180-198

  Query Match             28.6%;  Score 30;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

```
Sequence 198, Application US/11220856
; Publication No. US20060206962A1
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.DVUS02
;  CURRENT APPLICATION NUMBER: US/11/220,856
;  CURRENT FILING DATE:  2005-09-07
;  PRIOR APPLICATION NUMBER: US/10/658,180
;  PRIOR FILING DATE: 2003-09-09
;  PRIOR APPLICATION NUMBER: US 09/755,630
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-11-220-856-198

  Query Match             28.6%;  Score 30;  DB 7;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

```
I37261
complement receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I37261
R;Birkenbach, M.; Tong, X.; Bradbury, L.E.; Tedder, T.F.; Kieff, E.
J. Exp. Med. 176, 1405-1414, 1992
A;Title: Characterization of an Epstein-Barr virus receptor on human epithelial cells.
A;Reference number: I37261; MUID:93018869; PMID:1383386
A;Accession: I37261
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-27
A;Cross-references: UNIPROT:Q08578; UNIPARC:UPI0000072008; EMBL:X68990; NID:g3928195;
C;Genetics:
A;Gene: GDB:CR2
A;Cross-references: GDB:119802; OMIM:120650
A;Map position: 1q32-1q32

  Query Match             27.6%;  Score 29;  DB 2;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQ 11
              |||||:
Db          9 HYLRAR 14
```

```
Q4XXI0_PLACH
ID   Q4XXI0_PLACH   PRELIMINARY;   PRT;    25 AA.
AC   Q4XXI0;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Hypothetical protein (Fragment).
GN   ORFNames=PC104825.00.0;
OS   Plasmodium chabaudi.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5825;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15637271; DOI=10.1126/science.1103717;
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA   Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA   Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAJ01002442; CAH78381.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   25 AA;  2984 MW;  DD02DF108892E750 CRC64;

  Query Match             28.0%;  Score 28;  DB 2;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 6.9e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YVKKVN 7
              |||:||
Db         13 YVKRVN 18
```

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Q9UCK6_HUMAN
ID   Q9UCK6_HUMAN   PRELIMINARY;   PRT;    19 AA.
AC   Q9UCK6;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Aspartylglucosaminidase beta 1 subunit (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=93111925; PubMed=1281977;
RA   Rip J.W., Coulter-Mackie M.B., Rupar C.A., Gordon B.A.;
RT   "Purification and structure of human liver aspartylglucosaminidase.";
RL   Biochem. J. 288:1005-1010(1992).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   HSSP; P20933; 1APY.
SQ   SEQUENCE   19 AA;  2127 MW;  BC2F148525610300 CRC64;

  Query Match             27.0%;  Score 27;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KATEAA 13
              ||||||
Db         13 KATEAA 18
```

```
 Sequence 11, Application US/11136344
; Publication No. US20060178297A1
; GENERAL INFORMATION:
;  APPLICANT: Columbia University
;  APPLICANT:  Troy, Carol M.
;  APPLICANT:  Greene, Lloyd A.
;  TITLE OF INVENTION: SYSTEMS AND METHODS FOR SILENCING
;  TITLE OF INVENTION:  EXPRESSION OF A GENE IN A CELL AND USES THEREOF
;  FILE REFERENCE: 070050.2880
;  CURRENT APPLICATION NUMBER: US/11/136,344
;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: US 10/353,902
;  PRIOR FILING DATE: 2003-01-28
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MPS peptide is a chimera of the hydrophobic
;   OTHER INFORMATION: terminal domain of the viral gp41 protein and the
;   OTHER INFORMATION: nuclear localization signal from simian virus 40
;   OTHER INFORMATION: large antigen.
US-11-136-344-11

  Query Match             34.0%;  Score 34;  DB 7;  Length 27;
  Best Local Similarity   71.4%;  Pred. No. 52;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:||||:
Db          2 ALFLGWL 8
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```
Sequence 62, Application US/11474283
; Publication No. US20060234308A1
; GENERAL INFORMATION:
;  APPLICANT: Schneider-Mergener, Jens
;  APPLICANT:  Schutkowski, Mike
;  APPLICANT:  Reimer, Ulf
;  APPLICANT:  Dong, Liying
;  APPLICANT:  Panse, Soren
;  APPLICANT:  Scharn, Dirk
;  APPLICANT:  Osterkamp, Frank
;  APPLICANT:  Hummel, Gerd
;  APPLICANT:  Jobron, Laurence
;  TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymati
;  TITLE OF INVENTION:  Activity and a Device Therefor
;  FILE REFERENCE: 2918-0102
;  CURRENT APPLICATION NUMBER: US/11/474,283
;  CURRENT FILING DATE:  2006-06-26
;  PRIOR APPLICATION NUMBER: US/10/475,104
;  PRIOR FILING DATE: 2003-10-17
;  PRIOR APPLICATION NUMBER: PCT/EP02/04265
;  PRIOR FILING DATE: 2002-04-17
;  NUMBER OF SEQ ID NOS: 144
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: synthesized peptide sequence
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (2)..(2)
;   OTHER INFORMATION: Xaa = beta-alanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (12)..(12)
;   OTHER INFORMATION: amino group
US-11-474-283-62

  Query Match             25.0%;  Score 25;  DB 7;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 6.8e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 KKVNKATEAA 13
              ||:|:|   |
Db          3 KKLNRALAVA 12
```

```
Sequence 9, Application US/10144549
; Publication No. US20030211590A1
; GENERAL INFORMATION:
;  APPLICANT: GeneShuttle Biopharm, Inc.
;  APPLICANT:  Hwu , Paul  L.
;  TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
;  FILE REFERENCE: MBHB 02-340
;  CURRENT APPLICATION NUMBER: US/10/144,549
;  CURRENT FILING DATE:  2002-05-13
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: The fusion sequence of Gp41.
US-10-144-549-9

  Query Match             34.0%;  Score 34;  DB 4;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:||||:
Db          2 ALFLGWL 8
```

```
Sequence 288, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
;  APPLICANT: Brophy, Colleen
;  APPLICANT:  Komalavilas, Padmini
;  APPLICANT:  Panitch, Alyssa
;  APPLICANT:  Joshi, Lokesh
;  APPLICANT:  Seal, Brandon L.
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
;  FILE REFERENCE: ASU-1061-US
;  CURRENT APPLICATION NUMBER: US/10/226,956
;  CURRENT FILING DATE:  2002-08-23
;  PRIOR APPLICATION NUMBER: 60/314,535
;  PRIOR FILING DATE: 2001-08-23
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 288
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-226-956-288

  Query Match             34.0%;  Score 34;  DB 4;  Length 21;
  Best Local Similarity   71.4%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
```

```
Sequence 306, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
;  APPLICANT: Bright, Gary R.
;  APPLICANT:  Premkumar, D. David
;  APPLICANT:  Chen, Yih-Tai
;  TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular
;  FILE REFERENCE: 01-1022-US
;  CURRENT APPLICATION NUMBER: US/10/211,088
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/309,395
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/341,589
;  PRIOR FILING DATE: 2001-12-13
;  NUMBER OF SEQ ID NOS: 366
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 306
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Protein-derived transport peptide
US-10-211-088-306

  Query Match             34.0%;  Score 34;  DB 4;  Length 21;
  Best Local Similarity   71.4%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:||||:
Db          2 ALFLGWL 8
```

```
Sequence 8, Application US/09785802A
; Patent No. US20020151004A1
; GENERAL INFORMATION:
;  APPLICANT: Craig, Roger
;  TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
;  FILE REFERENCE: 11067/2035
;  CURRENT APPLICATION NUMBER: US/09/785,802A
;  CURRENT FILING DATE:  2001-02-16
;  PRIOR APPLICATION NUMBER: US 09/748,06
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/748,789
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
US-09-785-802A-8

  Query Match             34.0%;  Score 34;  DB 3;  Length 27;
  Best Local Similarity   71.4%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 AMFLGWV 19
               |:||||:
Db           2 ALFLGWL 8
```

```
Sequence 9, Application US/10144549
; Patent No. 6835810
; GENERAL INFORMATION:
;  APPLICANT: GeneShuttle Biopharm, Inc.
;  APPLICANT:  Hwu , Paul  L.
;  TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
;  FILE REFERENCE: MBHB 02-340
;  CURRENT APPLICATION NUMBER: US/10/144,549
;  CURRENT FILING DATE:  2002-05-13
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: The fusion sequence of Gp41.
US-10-144-549-9

  Query Match             34.0%;  Score 34;  DB 2;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 51;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
```

```
 Sequence 73, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 597-626)
US-10-715-810-73

  Query Match             58.0%;  Score 58;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ATEAAMFLGWV 19
              ||||||||||
Db          1 ATEAAMFLGWV 11
```

ADG28008
ID ADG28008 standard; peptide; 17 AA.
XX
AC ADG28008;
XX
DT 26-FEB-2004 (first entry)
XX
DE HIV1 gp41 membrane fusion sequence seq id 9.
XX
KW fusion protein; cold shock domain; membrane translocation sequence; CspA;
KW CspB; CspC; CspD; rp1 S1 binding domain; eukaryotic Y-box protein;
KW DNA binding protein B; DBPB; DBPA; EFE-1; mRNP3; mRNP4; FRG Y1;
KW nuclease-sensitive element binding protein 1; NSEP 1;
KW DNA condensation domain; DNA binding domain; SPKR;
KW nuclear localisation sequence; NLS; protein purification tagged sequence;
KW gene delivery; HIV1; gp41; membrane fusion sequence.
XX
OS Human immunodeficiency virus 1.
XX
PN US2003211590-A1.
XX
PD 13-NOV-2003.
XX
PF 13-MAY-2002; 2002US-00144549.
XX
PR 13-MAY-2002; 2002US-00144549.
XX
PA (HWUP/) HWU P L.
XX
PI Hwu PL;
XX
DR WPI; 2003-901590/82.
XX
PT New fusion protein comprising a cold shock domain, and a membrane
PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
PT cells for gene delivery.
XX
PS Claim 9; SEQ ID NO 9; 24pp; English.
XX
CC The invention describes a fusion protein for delivery of a desired
CC molecule into cells or nuclei, comprising a cold shock domain, its
CC homologue and functional derivative, and a membrane translocation
CC sequence or its functional equivalent peptides and/or derivatives. The
CC fusion protein comprises a cold shock domain that is selected from CspA,
CC CspB, CspC, CspD, rp1 S1 binding domain, eukaryotic Y-box proteins, DNA
CC binding protein B (DBPB), DBPA, EFE-1, mRNP3, mRNP4, FRG Y1 and nuclease-
CC sensitive element binding protein 1 (NSEP 1). The functional equivalent
CC derivative of cold shock protein is modified by inserting into the cold
CC shock domain with a DNA condensation domain or a DNA binding domain. The
CC DNA condensation or binding domain is selected from DNA condensation
CC domain (SPKR) 3-4 and the positive charge nuclear localisation sequences
CC (NLS+). The membrane transduction sequence is protein transduction domain
CC (PTD) or membrane fusion sequence. The fusion protein further comprises a
CC protein purification tagged sequence selected from HA, GST, and His6 tag.
CC The fusion protein is useful for delivering DNAs and RNAs to in vivo
CC cells for gene delivery, or for delivering nucleic acids to an embryo or
CC to a living animal for the production of transgenic animal. This is the
CC amino acid sequence of HIV1 gp41 membrane fusion sequence.
XX
SQ Sequence 17 AA;

```
  Query Match             34.0%;  Score 34;  DB 7;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 2.4e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
```

```
ABB77687
ID   ABB77687 standard; peptide; 27 AA.
XX
AC   ABB77687;
XX
DT   01-JUL-2002  (first entry)
XX
DE   New peptide vector#3.
XX
KW   Intracellular delivery; transfection agent; cancer; infectious disease;
KW   peptide vector.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 7
FT                   /note= "residue may be substituted with Phe"
FT   Misc-difference 23
FT                   /note= "residue may be substituted with Ser"
XX
PN   WO200210201-A2.
XX
PD   07-FEB-2002.
XX
PF   26-JUL-2001; 2001WO-US023406.
XX
PR   31-JUL-2000; 2000US-0221932P.
XX
PA   (ACTI-) ACTIVE MOTIF.
PA   (CNRS ) CENT NAT RECH SCI.
XX
PI   Divida G,  Morris M,  Mery J,  Heitz F,  Fernandez J,  Archdeacon J;
PI   Horndorp K;
XX
DR   WPI; 2002-329441/36.
XX
PT   Transfection agent that comprises a peptide comprising hydrophobic and
PT   hydrophilic domain and having amino acid residues of specified length is
PT   useful for a non-covalent association with and transport of a
PT   heterologous compound into a cell.
XX
PS   Example 2; Page 61; 156pp; English.
XX
CC   The invention relates to a transfection agent comprises a peptide of
CC   about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC   hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC   between the domains and a functional group conjugated to at least one
CC   terminal of the peptide. Peptides of the invention are useful for a non-
CC   covalent association with and transport of a heterologous compound into a
CC   cell. They are also useful for promoting the cellular internalisation of
CC   at least one member e.g. peptide, proteins, antibodies, their derivatives
CC   and/or conjugates. They may form part of a pharmaceutical composition to
CC   deliver the compound selected from a diagnostic or therapeutic compound,
CC   to treat at least one condition such as cancer or an infectious disease,
CC   or which targets a cancerous cell or pathogen-infected cell and to
CC   deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC   The agent of the invention has a transfection efficiency of at least 5%
CC   for at least two of the members of the group of the compounds. The agent
CC   has a good delivery efficiency for a broad spectrum of compounds and cell
CC   types, has a low toxicity, are easy to handle and easy to formulate in
CC   conjunction with the many different compound types that it can deliver.
```

CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents a
CC new amphipathic peptide vector of the invention that contains a cationic
CC nuclear localisation sequence
XX
SQ Sequence 27 AA;

Query Match 34.0%; Score 34; DB 5; Length 27;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
```

```
Q9S937_BETVU
ID   Q9S937_BETVU   PRELIMINARY;   PRT;    24 AA.
AC   Q9S937;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   H(+)-translocating (Pyrophosphate-ENERGIZED) inorganic pyrophosphatase
DE   beta-1 polypeptide (EC 3.6.1.1) (Fragment).
OS   Beta vulgaris (Sugar beet).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   Caryophyllales; Amaranthaceae; Beta.
OX   NCBI_TaxID=161934;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=92179265; PubMed=1311852;
RA   Sarafian V., Kim Y., Poole R.J., Rea P.A.;
RT   "Molecular cloning and sequence of cDNA encoding the pyrophosphate-
RT   energized vacuolar membrane proton pump of Arabidopsis thaliana.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   PIR; C38230; C38230.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. . .; IEA.
DR   GO; GO:0004427; F:inorganic diphosphatase activity; IEA.
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Sequence 4, Application US/11249692
; Publication No. US20060148009A1
; GENERAL INFORMATION:
;  APPLICANT: Barbosa, Maria D.F.S.
;  APPLICANT:  Chirino, Arthur J.
;  TITLE OF INVENTION: PREDICTION AND ASSESSMENT OF IMMUNOGENICITY
;  FILE REFERENCE: 185826/US/3 463077-396
;  CURRENT APPLICATION NUMBER: US/11/249,692
;  CURRENT FILING DATE:  2005-10-12
;  PRIOR APPLICATION NUMBER: US 60/659,586
;  PRIOR FILING DATE: 2005-03-08
;  PRIOR APPLICATION NUMBER: US 60/618,154
;  PRIOR FILING DATE: 2004-10-12
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-11-249-692-4

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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
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Perfect score: 99
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Scoring table: BLOSUM62
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Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 31 | 35 | 35.4 | 15 | 9 | ADY62780 | Ady62780 Ebola gly |
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| 33 | 35 | 35.4 | 16 | 6 | ABR40170 | Abr40170 Ebola vir |
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| 55 | 33 | 33.3 | 19 | 5 | ABJ04185 | Abj04185 Kinase-as |
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| 67 | 32 | 32.3 | 20 | 6 | ABJ19218 | Abj19218 T helper |
| 68 | 32 | 32.3 | 20 | 7 | ADD18054 | Add18054 Human G-p |
| 69 | 32 | 32.3 | 21 | 8 | ADL98131 | Adl98131 Candida k |
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| 124 | 30 | 30.3 | 12 | 2 | AAY08765 | Aay08765 Expressio |
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| 172 | 29 | 29.3 | 15 | 4 | AAG78631 | Aag78631 Plasmolem |
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| 174 | 29 | 29.3 | 15 | 5 | ABB83998 | Abb83998 Hydrogen |
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| 249 | 28 | 28.3 | 20 | 1 | AAP30118 | Aap30118 Sequence |
| 250 | 28 | 28.3 | 20 | 1 | AAP30321 | Aap30321 Sequence |
| 251 | 28 | 28.3 | 20 | 1 | AAP30121 | Aap30121 Sequence |
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| 255 | 28 | 28.3 | 20 | 5 | ABG75518 | Abg75518 HIV-1 p24 |
| 256 | 28 | 28.3 | 20 | 7 | ADC99540 | Adc99540 Cancer-re |

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| 257 | 28 | 28.3 | 20 | 7 | ADC99578 | Adc99578 Cancer-re |
| 258 | 28 | 28.3 | 20 | 7 | ADH37199 | Adh37199 Human lun |
| 259 | 28 | 28.3 | 20 | 8 | ABM79596 | Abm79596 M smegmat |
| 260 | 28 | 28.3 | 20 | 8 | ADN37727 | Adn37727 Human imm |
| 261 | 28 | 28.3 | 20 | 8 | ADI95349 | Adi95349 OSPF-rela |
| 262 | 28 | 28.3 | 20 | 8 | ADI95350 | Adi95350 OSPF-rela |
| 263 | 28 | 28.3 | 20 | 8 | ADI95351 | Adi95351 OSPF-rela |
| 264 | 28 | 28.3 | 20 | 9 | ADU98694 | Adu98694 Lung tumo |
| 265 | 28 | 28.3 | 20 | 9 | ADW98643 | Adw98643 HIV-1 str |
| 266 | 28 | 28.3 | 20 | 9 | ADW95664 | Adw95664 HIV-1 gro |
| 267 | 28 | 28.3 | 20 | 9 | ADY59301 | Ady59301 HIV-1 p24 |
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| 273 | 28 | 28.3 | 23 | 4 | AAU04333 | Aau04333 ATP-bindi |
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| 285 | 27.5 | 27.8 | 28 | 5 | AAU91198 | Aau91198 Human E1- |
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| 287 | 27.5 | 27.8 | 30 | 2 | AAR37008 | Aar37008 8-37 pept |
| 288 | 27.5 | 27.8 | 30 | 4 | AAB91150 | Aab91150 Pancreati |
| 289 | 27.5 | 27.8 | 30 | 4 | AAB91161 | Aab91161 Pancreati |
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| 291 | 27.5 | 27.8 | 30 | 4 | AAB91148 | Aab91148 Pancreati |
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| 293 | 27 | 27.3 | 7 | 8 | ADH56413 | Adh56413 Escherich |
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| 295 | 27 | 27.3 | 8 | 8 | ADH56416 | Adh56416 Escherich |
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| 297 | 27 | 27.3 | 9 | 4 | AAB47575 | Aab47575 Ag85 comp |
| 298 | 27 | 27.3 | 9 | 8 | ADP73819 | Adp73819 Loop inse |
| 299 | 27 | 27.3 | 9 | 8 | ADP25454 | Adp25454 Plasmodiu |
| 300 | 27 | 27.3 | 9 | 8 | ADT74321 | Adt74321 Human RSV |
| 301 | 27 | 27.3 | 9 | 8 | ADT73406 | Adt73406 Human RSV |
| 302 | 27 | 27.3 | 9 | 8 | ADT73404 | Adt73404 Human RSV |
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| 305 | 27 | 27.3 | 10 | 3 | ABP41032 | Abp41032 Human HER |
| 306 | 27 | 27.3 | 10 | 5 | ABG98942 | Abg98942 F protein |
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| 310 | 27 | 27.3 | 10 | 9 | ADW86248 | Adw86248 Human cal |
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| 314 | 27 | 27.3 | 11 | 4 | ABP23576 | Abp23576 HIV A11 m |
| 315 | 27 | 27.3 | 12 | 2 | AAW31289 | Aaw31289 Bovine be |
| 316 | 27 | 27.3 | 12 | 2 | AAW31290 | Aaw31290 Bovine be |
| 317 | 27 | 27.3 | 12 | 6 | AAO26477 | Aao26477 Debaryomy |

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| 318 | 27 | 27.3 | 12 | 7 | ADE41087 | Ade41087 Human Apo |
| 319 | 27 | 27.3 | 13 | 2 | AAR46640 | Aar46640 65 kD end |
| 320 | 27 | 27.3 | 13 | 5 | AAE27409 | Aae27409 Human gra |
| 321 | 27 | 27.3 | 13 | 5 | ADG66715 | Adg66715 Human CLC |
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| 324 | 27 | 27.3 | 13 | 5 | ADG65764 | Adg65764 Human G-C |
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| 326 | 27 | 27.3 | 13 | 7 | ADJ62461 | Adj62461 Tryptic s |
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| 328 | 27 | 27.3 | 14 | 2 | AAR60917 | Aar60917 TSST-1 am |
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| 330 | 27 | 27.3 | 15 | 4 | AAB99900 | Aab99900 Human fib |
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| 332 | 27 | 27.3 | 15 | 4 | ABP24672 | Abp24672 HIV DR su |
| 333 | 27 | 27.3 | 15 | 8 | ADU64294 | Adu64294 32 KD pro |
| 334 | 27 | 27.3 | 15 | 9 | ADV22459 | Adv22459 HIV-1 Pol |
| 335 | 27 | 27.3 | 15 | 9 | ADV23616 | Adv23616 HBV immun |
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| 337 | 27 | 27.3 | 15 | 9 | ADV22458 | Adv22458 HIV-1 Pol |
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| 339 | 27 | 27.3 | 15 | 9 | AEC13981 | Aec13981 E. faecal |
| 340 | 27 | 27.3 | 16 | 7 | ADF92403 | Adf92403 Human ubi |
| 341 | 27 | 27.3 | 16 | 9 | ADW98372 | Adw98372 Alpha2 53 |
| 342 | 27 | 27.3 | 16 | 9 | ADW98447 | Adw98447 Alpha2 53 |
| 343 | 27 | 27.3 | 17 | 3 | AAB44353 | Aab44353 Human sec |
| 344 | 27 | 27.3 | 17 | 10 | AEG01060 | Aeg01060 Kallikrei |
| 345 | 27 | 27.3 | 17 | 10 | AEG02788 | Aeg02788 Anti-ghre |
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| 347 | 27 | 27.3 | 18 | 9 | AEB77708 | Aeb77708 Casomorph |
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| 351 | 27 | 27.3 | 19 | 8 | ADK49226 | Adk49226 Human car |
| 352 | 27 | 27.3 | 19 | 8 | ADK50650 | Adk50650 Human car |
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| 354 | 27 | 27.3 | 19 | 9 | AEC91525 | Aec91525 IFN-gamma |
| 355 | 27 | 27.3 | 20 | 2 | AAR74662 | Aar74662 Pseudomon |
| 356 | 27 | 27.3 | 20 | 5 | AAE25787 | Aae25787 Aspergill |
| 357 | 27 | 27.3 | 20 | 5 | ABB04309 | Abb04309 Human PGI |
| 358 | 27 | 27.3 | 20 | 9 | ADW52403 | Adw52403 Human PL |
| 359 | 27 | 27.3 | 21 | 7 | ADM56162 | Adm56162 C. tracho |
| 360 | 27 | 27.3 | 21 | 8 | ADQ76682 | Adq76682 Aprotinin |
| 361 | 27 | 27.3 | 22 | 3 | AAB53228 | Aab53228 Protein c |
| 362 | 27 | 27.3 | 22 | 4 | AAM18517 | Aam18517 Peptide # |
| 363 | 27 | 27.3 | 22 | 4 | ABB32293 | Abb32293 Peptide # |
| 364 | 27 | 27.3 | 22 | 8 | ADH76534 | Adh76534 Human neu |
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| 366 | 27 | 27.3 | 22 | 8 | AEE67082 | Aee67082 Cancer tr |
| 367 | 27 | 27.3 | 23 | 4 | AAB50161 | Aab50161 Human bra |
| 368 | 27 | 27.3 | 23 | 4 | AAB48158 | Aab48158 Human MCH |
| 369 | 27 | 27.3 | 24 | 2 | AAR36998 | Aar36998 Amylin an |
| 370 | 27 | 27.3 | 24 | 2 | AAR36999 | Aar36999 Ac-24Ser, |
| 371 | 27 | 27.3 | 24 | 2 | AAR37000 | Aar37000 Adamantyl |
| 372 | 27 | 27.3 | 24 | 2 | AAY49524 | Aay49524 HIV resis |
| 373 | 27 | 27.3 | 24 | 3 | AAB01926 | Aab01926 Drosophil |
| 374 | 27 | 27.3 | 24 | 6 | ABG74323 | Abg74323 Fruitfly |
| 375 | 27 | 27.3 | 24 | 9 | AEB95963 | Aeb95963 Human MCH |
| 376 | 27 | 27.3 | 25 | 2 | AAR36997 | Aar36997 Amylin an |
| 377 | 27 | 27.3 | 25 | 2 | AAR68758 | Aar68758 Cytotoxic |
| 378 | 27 | 27.3 | 25 | 2 | AAW32895 | Aaw32895 HIV pol p |

| | | | | | | |
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| 379 | 27 | 27.3 | 25 | 3 | AAB13242 | Aab13242 Ascoris s |
| 380 | 27 | 27.3 | 25 | 4 | AAM21747 | Aam21747 Peptide # |
| 381 | 27 | 27.3 | 25 | 4 | ABB44116 | Abb44116 Peptide # |
| 382 | 27 | 27.3 | 25 | 4 | AAM38063 | Aam38063 Peptide # |
| 383 | 27 | 27.3 | 25 | 4 | ABB27003 | Abb27003 Protein # |
| 384 | 27 | 27.3 | 25 | 4 | AAM77843 | Aam77843 Human bon |
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| 386 | 27 | 27.3 | 25 | 4 | ABG59498 | Abg59498 Human liv |
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| 388 | 27 | 27.3 | 25 | 5 | ABG46871 | Abg46871 Human pep |
| 389 | 27 | 27.3 | 25 | 5 | ABG62245 | Abg62245 Eubacteri |
| 390 | 27 | 27.3 | 25 | 5 | ABG68684 | Abg68684 HIV-1 P21 |
| 391 | 27 | 27.3 | 25 | 7 | ADB47951 | Adb47951 Novel hum |
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| 394 | 27 | 27.3 | 25 | 9 | AED67489 | Aed67489 Human pep |
| 395 | 27 | 27.3 | 25 | 10 | AEE38542 | Aee38542 Human ser |
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| 397 | 27 | 27.3 | 26 | 2 | AAY36392 | Aay36392 Fragment |
| 398 | 27 | 27.3 | 26 | 3 | AAY87534 | Aay87534 Mature co |
| 399 | 27 | 27.3 | 26 | 5 | AAU81826 | Aau81826 Phosphino |
| 400 | 27 | 27.3 | 26 | 6 | ADA11851 | Ada11851 Human nov |
| 401 | 27 | 27.3 | 26 | 8 | ADP86220 | Adp86220 P2Y2 or P |
| 402 | 27 | 27.3 | 27 | 2 | AAR58337 | Aar58337 Hypotensi |
| 403 | 27 | 27.3 | 27 | 8 | ADG37022 | Adg37022 Bovine ca |
| 404 | 27 | 27.3 | 28 | 1 | AAP91574 | Aap91574 Sequence |
| 405 | 27 | 27.3 | 28 | 2 | AAW57151 | Aaw57151 Measles v |
| 406 | 27 | 27.3 | 28 | 2 | AAW57166 | Aaw57166 Measles v |
| 407 | 27 | 27.3 | 29 | 2 | AAW78272 | Aaw78272 Fragment |
| 408 | 27 | 27.3 | 29 | 3 | AAY91260 | Aay91260 Modified |
| 409 | 27 | 27.3 | 29 | 4 | AAM19736 | Aam19736 Peptide # |
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| 411 | 27 | 27.3 | 29 | 4 | AAM33018 | Aam33018 Peptide # |
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| 417 | 27 | 27.3 | 29 | 8 | ADL97675 | Adl97675 Protein e |
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| 419 | 27 | 27.3 | 29 | 8 | ADK50651 | Adk50651 Human car |
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| 421 | 27 | 27.3 | 30 | 2 | AAY14184 | Aay14184 HCV envel |
| 422 | 27 | 27.3 | 30 | 5 | ABJ10342 | Abj10342 Human lun |
| 423 | 27 | 27.3 | 30 | 5 | AAU84454 | Aau84454 HIV POL s |
| 424 | 27 | 27.3 | 30 | 5 | AAU84453 | Aau84453 HIV POL s |
| 425 | 27 | 27.3 | 30 | 8 | ADT39600 | Adt39600 hSARS vir |
| 426 | 27 | 27.3 | 30 | 8 | ADS79019 | Ads79019 SARS viru |
| 427 | 27 | 27.3 | 30 | 8 | ADT37130 | Adt37130 hSARS vir |
| 428 | 27 | 27.3 | 30 | 9 | AEA22177 | Aea22177 Campyloba |
| 429 | 26.5 | 26.8 | 10 | 2 | AAR53621 | Aar53621 Opioid pe |
| 430 | 26.5 | 26.8 | 10 | 2 | AAR89234 | Aar89234 SC clone |
| 431 | 26.5 | 26.8 | 18 | 8 | ADK50707 | Adk50707 Human car |
| 432 | 26.5 | 26.8 | 20 | 6 | ABP72139 | Abp72139 Bombina m |
| 433 | 26.5 | 26.8 | 22 | 2 | AAW96827 | Aaw96827 Nucleic a |
| 434 | 26.5 | 26.8 | 24 | 3 | AAB18711 | Aab18711 Synthetic |
| 435 | 26.5 | 26.8 | 24 | 3 | AAB18697 | Aab18697 Synthetic |
| 436 | 26.5 | 26.8 | 24 | 8 | ADR84154 | Adr84154 S. pyogen |
| 437 | 26.5 | 26.8 | 26 | 2 | AAR14987 | Aar14987 Part of e |
| 438 | 26.5 | 26.8 | 27 | 8 | ADK50708 | Adk50708 Human car |
| 439 | 26.5 | 26.8 | 27 | 10 | AEE38928 | Aee38928 Human ser |

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| 441 | 26.5 | 26.8 | 28 | 2 | AAR14974 | Aar14974 Part of e |
| 442 | 26.5 | 26.8 | 29 | 5 | AAU91200 | Aau91200 Human E1- |
| 443 | 26.5 | 26.8 | 29 | 5 | AAU91199 | Aau91199 Human E1- |
| 444 | 26.5 | 26.8 | 29 | 8 | ADI79971 | Adi79971 E1-E2 ATP |
| 445 | 26.5 | 26.8 | 29 | 8 | ADI79970 | Adi79970 E1-E2 ATP |
| 446 | 26 | 26.3 | 5 | 6 | ABU12136 | Abu12136 Bovine BP |
| 447 | 26 | 26.3 | 7 | 4 | AAB49618 | Aab49618 HIV-1 int |
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| 449 | 26 | 26.3 | 7 | 9 | AEC17851 | Aec17851 Casein pe |
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| 451 | 26 | 26.3 | 8 | 2 | AAR25088 | Aar25088 bGRF prod |
| 452 | 26 | 26.3 | 8 | 4 | AAB82743 | Aab82743 Peptide c |
| 453 | 26 | 26.3 | 8 | 8 | ADK38411 | Adk38411 Hepatitis |
| 454 | 26 | 26.3 | 8 | 9 | ADZ05801 | Adz05801 Hepatitis |
| 455 | 26 | 26.3 | 8 | 9 | AEC17623 | Aec17623 Casein pe |
| 456 | 26 | 26.3 | 8 | 9 | AEC17622 | Aec17622 Casein pe |
| 457 | 26 | 26.3 | 8 | 9 | AEC17863 | Aec17863 Casein pe |
| 458 | 26 | 26.3 | 8 | 9 | AEC17864 | Aec17864 Casein pe |
| 459 | 26 | 26.3 | 9 | 2 | AAR59233 | Aar59233 Peptide f |
| 460 | 26 | 26.3 | 9 | 2 | AAR53607 | Aar53607 Opioid pe |
| 461 | 26 | 26.3 | 9 | 2 | AAR70067 | Aar70067 Control p |
| 462 | 26 | 26.3 | 9 | 2 | AAW54515 | Aaw54515 Synthetic |
| 463 | 26 | 26.3 | 9 | 4 | AAE11834 | Aae11834 Mycobacte |
| 464 | 26 | 26.3 | 9 | 5 | ABJ07523 | Abj07523 Hepatitis |
| 465 | 26 | 26.3 | 9 | 5 | ABJ08794 | Abj08794 Hepatitis |
| 466 | 26 | 26.3 | 9 | 5 | ABJ06013 | Abj06013 Hepatitis |
| 467 | 26 | 26.3 | 9 | 5 | ABJ09086 | Abj09086 Hepatitis |
| 468 | 26 | 26.3 | 9 | 6 | ADA51191 | Ada51191 Rous sarc |
| 469 | 26 | 26.3 | 9 | 7 | ABW00526 | Abw00526 Human cyt |
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| 471 | 26 | 26.3 | 9 | 8 | ADE97695 | Ade97695 Immunogen |
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| 473 | 26 | 26.3 | 9 | 8 | ADK38403 | Adk38403 Hepatitis |
| 474 | 26 | 26.3 | 9 | 8 | ADK37320 | Adk37320 Hepatitis |
| 475 | 26 | 26.3 | 9 | 8 | ADO01394 | Ado01394 Human cyt |
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| 478 | 26 | 26.3 | 9 | 8 | ADR22332 | Adr22332 Anti-Hepa |
| 479 | 26 | 26.3 | 9 | 8 | ADR11427 | Adr11427 Hepatitis |
| 480 | 26 | 26.3 | 9 | 8 | ADT73405 | Adt73405 Human RSV |
| 481 | 26 | 26.3 | 9 | 8 | ADT73183 | Adt73183 Human RSV |
| 482 | 26 | 26.3 | 9 | 8 | ADT73184 | Adt73184 Human RSV |
| 483 | 26 | 26.3 | 9 | 8 | ADT72243 | Adt72243 Human RSV |
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| 485 | 26 | 26.3 | 9 | 9 | ADZ05793 | Adz05793 Hepatitis |
| 486 | 26 | 26.3 | 9 | 9 | ADZ06052 | Adz06052 Hepatitis |
| 487 | 26 | 26.3 | 9 | 9 | ADZ04710 | Adz04710 Hepatitis |
| 488 | 26 | 26.3 | 9 | 9 | ADZ57115 | Adz57115 Cytotoxic |
| 489 | 26 | 26.3 | 9 | 9 | AEC17642 | Aec17642 Casein pe |
| 490 | 26 | 26.3 | 9 | 9 | AEC17876 | Aec17876 Casein pe |
| 491 | 26 | 26.3 | 9 | 9 | AEC17640 | Aec17640 Casein pe |
| 492 | 26 | 26.3 | 9 | 9 | AEC17874 | Aec17874 Casein pe |
| 493 | 26 | 26.3 | 9 | 9 | AEC17875 | Aec17875 Casein pe |
| 494 | 26 | 26.3 | 9 | 9 | AEC17641 | Aec17641 Casein pe |
| 495 | 26 | 26.3 | 10 | 2 | AAR25103 | Aar25103 bGRF prod |
| 496 | 26 | 26.3 | 10 | 2 | AAR25091 | Aar25091 bGRF prod |
| 497 | 26 | 26.3 | 10 | 2 | AAR57928 | Aar57928 Randomly |
| 498 | 26 | 26.3 | 10 | 2 | AAR63343 | Aar63343 Peptide f |
| 499 | 26 | 26.3 | 10 | 2 | AAR57875 | Aar57875 Viral hea |
| 500 | 26 | 26.3 | 10 | 2 | AAR53608 | Aar53608 Opioid pe |

| | | | | | | |
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| 501 | 26 | 26.3 | 10 | 2 | AAR53618 | Aar53618 Opioid pe |
| 502 | 26 | 26.3 | 10 | 2 | AAR96501 | Aar96501 Hepatitis |
| 503 | 26 | 26.3 | 10 | 2 | AAW32216 | Aaw32216 Alpha-S2 |
| 504 | 26 | 26.3 | 10 | 3 | AAY94204 | Aay94204 Human cyt |
| 505 | 26 | 26.3 | 10 | 4 | AAB72516 | Aab72516 Colostrin |
| 506 | 26 | 26.3 | 10 | 4 | AAB59326 | Aab59326 Ewe colos |
| 507 | 26 | 26.3 | 10 | 4 | AAB72263 | Aab72263 Colostrin |
| 508 | 26 | 26.3 | 10 | 4 | AAB72548 | Aab72548 Colostrin |
| 509 | 26 | 26.3 | 10 | 4 | AAG78080 | Aag78080 PB(III) m |
| 510 | 26 | 26.3 | 10 | 4 | AAB66835 | Aab66835 Metal ion |
| 511 | 26 | 26.3 | 10 | 4 | AAE11846 | Aae11846 M. tuberc |

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Sequence 4, Application US/10603094
; Publication No. US20040101534A1
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don
;  TITLE OF INVENTION: ADJUVANT-FREE PEPTIDE VACCINE
;  FILE REFERENCE: 1954-410
;  CURRENT APPLICATION NUMBER: US/10/603,094
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: US 60/391088
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Tetanus
US-10-603-094-4

  Query Match             56.6%;  Score 56;  DB 4;  Length 14;
  Best Local Similarity   90.9%;  Pred. No. 0.05;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
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Db          4 IVPYIGPALNI 14
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 Sequence 19, Application US/09984365
; Publication No. US20030224980A1
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don J
;  TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
;  FILE REFERENCE: 1954-384
;  CURRENT APPLICATION NUMBER: US/09/984,365
;  CURRENT FILING DATE:  2002-03-13
;  PRIOR APPLICATION NUMBER: US 09/692170
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 09/534639
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 09/075257
;  PRIOR FILING DATE: 1998-05-11
;  PRIOR APPLICATION NUMBER: US 09/021298
;  PRIOR FILING DATE: 1998-02-10
;  PRIOR APPLICATION NUMBER: US 08/950064
;  PRIOR FILING DATE: 1997-10-14
;  PRIOR APPLICATION NUMBER: US 08/747488
;  PRIOR FILING DATE: 1996-11-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HCMV vaccine peptide
US-09-984-365-19

  Query Match             56.6%;  Score 56;  DB 3;  Length 26;
  Best Local Similarity   90.9%;  Pred. No. 0.097;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
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Db          4 IVPYIGPALNI 14
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 Sequence 7, Application US/10603094
; Publication No. US20040101534A1
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don
;  TITLE OF INVENTION: ADJUVANT-FREE PEPTIDE VACCINE
;  FILE REFERENCE: 1954-410
;  CURRENT APPLICATION NUMBER: US/10/603,094
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: US 60/391088
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: KTet639V fusion peptide
US-10-603-094-7

  Query Match             56.6%;  Score 56;  DB 4;  Length 26;
  Best Local Similarity   90.9%;  Pred. No. 0.097;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:|||||||||
Db          4 IVPYIGPALNI 14
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Sequence 44, Application US/08446692
; Patent No. 5759551
;  GENERAL INFORMATION:
;    APPLICANT:  Ladd, Anna
;    APPLICANT:  Wang, Chang Yi
;    APPLICANT:  Zamb, Timothy
;    TITLE OF INVENTION:  Immunogenic LHRH peptide constructs
;    TITLE OF INVENTION:  and synthetic universal immune stimulators for vaccines
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maria C.H. Lin
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,692
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria C.H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4146 US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)415-8745
;      TELEFAX:  (516)751-6849
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-446-692-44

  Query Match             56.6%;  Score 56;  DB 1;  Length 16;
  Best Local Similarity   90.9%;  Pred. No. 0.081;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
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Db          5 IVPYIGPALNI 15
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Sequence 73, Application PC/TUS9311703
;  GENERAL INFORMATION:
;    APPLICANT:  Chiron Mimotopes Pty. Ltd.
;    TITLE OF INVENTION:  T-Cell Epitopes
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Grant D. Green
;      STREET:  4560 Horton St.
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/11703
;      FILING DATE:  28-DEC-1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984,852
;      FILING DATE:  02-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Grant D.
;      REGISTRATION NUMBER:  31,259
;      REFERENCE/DOCKET NUMBER:  0222.101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-601-2706
;      TELEFAX:  510-655-3542
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-11703-73

  Query Match             42.4%;  Score 42;  DB 5;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPA 10
              |:||||||
Db          1 IVPYIGPA 8
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Sequence 10357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10357
;  LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-10357

  Query Match             30.3%;  Score 30;  DB 2;  Length 30;
  Best Local Similarity   66.7%;  Pred. No. 1e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IPYIGP 9
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Db         13 VPFIGP 18
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Sequence 19, Application US/09984365
; Patent No. 6733973
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don J
;  TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
;  FILE REFERENCE: 1954-384
;  CURRENT APPLICATION NUMBER: US/09/984,365
;  CURRENT FILING DATE:  2002-03-13
;  PRIOR APPLICATION NUMBER: US 09/692170
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 09/534639
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 09/075257
;  PRIOR FILING DATE: 1998-05-11
;  PRIOR APPLICATION NUMBER: US 09/021298
;  PRIOR FILING DATE: 1998-02-10
;  PRIOR APPLICATION NUMBER: US 08/950064
;  PRIOR FILING DATE: 1997-10-14
;  PRIOR APPLICATION NUMBER: US 08/747488
;  PRIOR FILING DATE: 1996-11-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HCMV vaccine peptide
US-09-984-365-19

  Query Match             56.6%;  Score 56;  DB 2;  Length 26;
  Best Local Similarity   90.9%;  Pred. No. 0.13;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:||||||||||
Db          4 IVPYIGPALNI 14
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Sequence 19, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
;  APPLICANT: Chain, Benjamin
;  TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHOD
;  TITLE OF INVENTION:  FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
;  FILE REFERENCE: 20555/1203433-US1
;  CURRENT APPLICATION NUMBER: US/09/731,899
;  CURRENT FILING DATE:  2000-12-08
;  PRIOR APPLICATION NUMBER: 60/169,687
;  PRIOR FILING DATE: 1999-12-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Tetanus toxin bacteria
US-09-731-899-19
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631-649

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  Query Match             52.5%;  Score 52;  DB 1;  Length 16;
  Best Local Similarity   90.0%;  Pred. No. 0.031;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALN 12
              |:||||||||
Db          5 IVPYIGPALN 14
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GenCore version 5.1.9


OM protein - protein search, using sw model

Run on: November 1, 2006, 12:30:50 ; Search time 99.3 Seconds
(without alignments)
176.992 Million cell updates/sec

Title: US-10-821-669-1_COPY_631_649
Perfect score: 99
Sequence: 1 TIIIPYIGPALNIGNMLYK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 37 | 37.4 | 13 | 1 | CRBL_ICASP | P17237 icaria sp. |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_673_691
Perfect score: 91
Sequence: 1 IPVLGTFALVSYIANKVLT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 91 | 100.0 | 27 | 9 | ADW11111 | Adw11111 Clostridi |
| 3 | 44 | 48.4 | 27 | 9 | ADW11110 | Adw11110 Clostridi |
| 4 | 43 | 47.3 | 27 | 9 | ADW11112 | Adw11112 Clostridi |
| 5 | 34 | 37.4 | 16 | 9 | AEB21004 | Aeb21004 Aspartate |
| 6 | 34 | 37.4 | 16 | 9 | AEB21006 | Aeb21006 Aspartate |
| 7 | 34 | 37.4 | 21 | 9 | AEB21007 | Aeb21007 Aspartate |
| 8 | 34 | 37.4 | 21 | 9 | AEB21005 | Aeb21005 Aspartate |
| 9 | 34 | 37.4 | 28 | 8 | ABO54884 | Abo54884 Human gen |
| 10 | 33 | 36.3 | 21 | 2 | AAY17917 | Aay17917 Vesicle t |
| 11 | 32 | 35.2 | 15 | 2 | AAR13976 | Aar13976 [Phe14]Me |
| 12 | 32 | 35.2 | 15 | 2 | AAR61467 | Aar61467 [Phe- or |

| | | | | | | |
|---|---|---|---|---|---|---|
| 13 | 32 | 35.2 | 20 | 9 | ADZ98557 | Adz98557 Human ami |
| 14 | 32 | 35.2 | 20 | 9 | ADZ98558 | Adz98558 Human ami |
| 15 | 32 | 35.2 | 27 | 5 | ABB89007 | Abb89007 Babesia m |
| 16 | 32 | 35.2 | 27 | 7 | ADE06135 | Ade06135 BMNI-rela |
| 17 | 32 | 35.2 | 30 | 10 | AEE38707 | Aee38707 Human ser |
| 18 | 31 | 34.1 | 10 | 6 | ABR05207 | Abr05207 Human can |
| 19 | 31 | 34.1 | 15 | 6 | ABR31075 | Abr31075 Human can |
| 20 | 31 | 34.1 | 15 | 6 | ABR30903 | Abr30903 Human can |
| 21 | 31 | 34.1 | 15 | 6 | ABR30578 | Abr30578 Human can |
| 22 | 31 | 34.1 | 15 | 6 | ABR31050 | Abr31050 Human can |
| 23 | 31 | 34.1 | 15 | 6 | ABR31300 | Abr31300 Human can |
| 24 | 31 | 34.1 | 15 | 6 | ABR30718 | Abr30718 Human can |
| 25 | 31 | 34.1 | 15 | 6 | ABR31535 | Abr31535 Human can |
| 26 | 31 | 34.1 | 15 | 6 | ABR30976 | Abr30976 Human can |
| 27 | 31 | 34.1 | 15 | 6 | ABR31454 | Abr31454 Human can |
| 28 | 31 | 34.1 | 15 | 6 | ABR31586 | Abr31586 Human can |
| 29 | 31 | 34.1 | 15 | 6 | ABR31076 | Abr31076 Human can |
| 30 | 31 | 34.1 | 15 | 7 | ADE00896 | Ade00896 Human 193 |
| 31 | 31 | 34.1 | 15 | 7 | ADE00705 | Ade00705 Human 193 |
| 32 | 31 | 34.1 | 15 | 7 | ADE01050 | Ade01050 Human 193 |
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| 34 | 31 | 34.1 | 15 | 8 | ADP53502 | Adp53502 Human 193 |
| 35 | 31 | 34.1 | 15 | 8 | ADP53693 | Adp53693 Human 193 |
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| 37 | 31 | 34.1 | 16 | 7 | ABM74151 | Abm74151 DNA clone |
| 38 | 31 | 34.1 | 19 | 2 | AAY42677 | Aay42677 HHV-6 var |
| 39 | 31 | 34.1 | 21 | 9 | AEB21013 | Aeb21013 Aspartate |
| 40 | 31 | 34.1 | 26 | 2 | AAR27267 | Aar27267 Signal pe |
| 41 | 31 | 34.1 | 28 | 10 | AEE36906 | Aee36906 Human ser |
| 42 | 30 | 33.0 | 10 | 8 | ADK08573 | Adk08573 Human pap |
| 43 | 30 | 33.0 | 10 | 8 | ADK08574 | Adk08574 Human pap |
| 44 | 30 | 33.0 | 13 | 9 | ADX17310 | Adx17310 Human ser |
| 45 | 30 | 33.0 | 15 | 2 | AAR13129 | Aar13129 GPIb alph |
| 46 | 30 | 33.0 | 15 | 2 | AAY55128 | Aay55128 ATCC HB 1 |
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| 48 | 30 | 33.0 | 15 | 9 | AEB25836 | Aeb25836 Peptide O |
| 49 | 30 | 33.0 | 17 | 2 | AAR90401 | Aar90401 Antibody |
| 50 | 30 | 33.0 | 17 | 8 | ADS13418 | Ads13418 Human rhe |
| 51 | 30 | 33.0 | 19 | 10 | AEE39244 | Aee39244 Human ser |
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| 54 | 30 | 33.0 | 23 | 9 | ADV56511 | Adv56511 G protein |
| 55 | 30 | 33.0 | 25 | 2 | AAY12585 | Aay12585 Human 5' |
| 56 | 30 | 33.0 | 25 | 4 | AAB65845 | Aab65845 Murine IN |
| 57 | 30 | 33.0 | 26 | 2 | AAR38829 | Aar38829 Melittin |
| 58 | 30 | 33.0 | 27 | 4 | AAE01286 | Aae01286 Human gen |
| 59 | 30 | 33.0 | 27 | 5 | AAU80425 | Aau80425 Positive |
| 60 | 30 | 33.0 | 27 | 5 | ABG63719 | Abg63719 Human alb |
| 61 | 30 | 33.0 | 27 | 8 | ADL76984 | Adl76984 Albumin f |
| 62 | 30 | 33.0 | 28 | 9 | ADV91110 | Adv91110 Sodium ch |
| 63 | 30 | 33.0 | 28 | 9 | ADX69229 | Adx69229 Voltage-g |
| 64 | 30 | 33.0 | 30 | 9 | AEB95955 | Aeb95955 Human mel |
| 65 | 29.5 | 32.4 | 19 | 6 | ABU13492 | Abu13492 Zona pell |
| 66 | 29 | 31.9 | 10 | 4 | AAG87763 | Aag87763 Saccharom |
| 67 | 29 | 31.9 | 10 | 4 | AAG87762 | Aag87762 Saccharom |
| 68 | 29 | 31.9 | 11 | 9 | ADV50819 | Adv50819 Murine br |
| 69 | 29 | 31.9 | 13 | 5 | AAE27595 | Aae27595 Human bet |
| 70 | 29 | 31.9 | 13 | 5 | AAE27594 | Aae27594 Human bet |
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| 74 | 29 | 31.9 | 15 | 10 | AEE39065 | Aee39065 Human ser |
| 75 | 29 | 31.9 | 19 | 5 | ABG79262 | Abg79262 Human K+a |
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| 77 | 29 | 31.9 | 20 | 8 | ADI41254 | Adi41254 Human HGP |
| 78 | 29 | 31.9 | 20 | 8 | ADI41294 | Adi41294 Human HGP |
| 79 | 29 | 31.9 | 20 | 9 | ADW81161 | Adw81161 AMPK modu |
| 80 | 29 | 31.9 | 20 | 9 | ADW81192 | Adw81192 AMPK modu |
| 81 | 29 | 31.9 | 20 | 10 | AEF14752 | Aef14752 Human cho |
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| 85 | 29 | 31.9 | 25 | 2 | AAR49587 | Aar49587 Sequence |
| 86 | 29 | 31.9 | 25 | 2 | AAW31864 | Aaw31864 MHC class |
| 87 | 29 | 31.9 | 25 | 2 | AAY09341 | Aay09341 Human pap |
| 88 | 29 | 31.9 | 25 | 3 | AAY70694 | Aay70694 Endoplasm |
| 89 | 29 | 31.9 | 25 | 3 | AAB30292 | Aab30292 CD4+ T-ce |
| 90 | 29 | 31.9 | 25 | 4 | AAG67288 | Aag67288 Amino aci |
| 91 | 29 | 31.9 | 25 | 4 | AAB95956 | Aab95956 HLA-DRalp |
| 92 | 29 | 31.9 | 25 | 4 | AAG64714 | Aag64714 HPV immun |
| 93 | 29 | 31.9 | 25 | 4 | AAB20205 | Aab20205 HLA-DR-al |
| 94 | 29 | 31.9 | 25 | 4 | AAU03561 | Aau03561 Hydrophob |
| 95 | 29 | 31.9 | 25 | 5 | AAO17006 | Aao17006 HLA-Dralp |
| 96 | 29 | 31.9 | 25 | 5 | ABG68880 | Abg68880 Endoplasm |
| 97 | 29 | 31.9 | 25 | 5 | AAE19014 | Aae19014 Hydrophob |
| 98 | 29 | 31.9 | 25 | 5 | ABB09908 | Abb09908 Radiolabe |
| 99 | 29 | 31.9 | 25 | 5 | ABB75927 | Abb75927 Endoplasm |
| 100 | 29 | 31.9 | 25 | 5 | ABB08107 | Abb08107 MHC class |
| 101 | 29 | 31.9 | 25 | 6 | ABU08975 | Abu08975 Human exp |
| 102 | 29 | 31.9 | 25 | 6 | AAE35568 | Aae35568 Hydrophob |
| 103 | 29 | 31.9 | 25 | 6 | AAO23269 | Aao23269 Hydrophob |
| 104 | 29 | 31.9 | 25 | 6 | ABU63379 | Abu63379 Human tPA |
| 105 | 29 | 31.9 | 25 | 7 | ABU10009 | Abu10009 Human leu |
| 106 | 29 | 31.9 | 25 | 7 | ADF57571 | Adf57571 Human sig |
| 107 | 29 | 31.9 | 25 | 8 | ADM13766 | Adm13766 MHC class |
| 108 | 29 | 31.9 | 25 | 8 | ADN59204 | Adn59204 HLA-DRalp |
| 109 | 29 | 31.9 | 25 | 8 | ADU47822 | Adu47822 HPV strai |
| 110 | 29 | 31.9 | 25 | 9 | ADV99799 | Adv99799 Glucanase |
| 111 | 29 | 31.9 | 25 | 10 | AEE64440 | Aee64440 Human HLA |
| 112 | 29 | 31.9 | 25 | 10 | AEF53024 | Aef53024 Signal pe |
| 113 | 29 | 31.9 | 25 | 10 | AEF24307 | Aef24307 Endoplasm |
| 114 | 29 | 31.9 | 26 | 4 | AAB50207 | Aab50207 Membrane |
| 115 | 29 | 31.9 | 29 | 5 | ABG79237 | Abg79237 Human K+a |
| 116 | 29 | 31.9 | 29 | 5 | ABG68893 | Abg68893 Secretion |
| 117 | 29 | 31.9 | 30 | 2 | AAY29969 | Aay29969 C. elegan |
| 118 | 29 | 31.9 | 30 | 2 | AAY29968 | Aay29968 C. elegan |
| 119 | 28.5 | 31.3 | 18 | 10 | AEF71020 | Aef71020 Human int |
| 120 | 28.5 | 31.3 | 27 | 8 | ADM97975 | Adm97975 Sesquiter |
| 121 | 28 | 30.8 | 9 | 6 | ABR05322 | Abr05322 Human can |
| 122 | 28 | 30.8 | 10 | 6 | ABJ38163 | Abj38163 Human cyt |
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| 124 | 28 | 30.8 | 15 | 7 | ADE00690 | Ade00690 Human 193 |
| 125 | 28 | 30.8 | 15 | 7 | ADE00750 | Ade00750 Human 193 |
| 126 | 28 | 30.8 | 15 | 7 | ADE00938 | Ade00938 Human 193 |
| 127 | 28 | 30.8 | 15 | 7 | ADE00976 | Ade00976 Human 193 |
| 128 | 28 | 30.8 | 15 | 8 | ADP53773 | Adp53773 Human 193 |
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| 131 | 28 | 30.8 | 15 | 8 | ADP53547 | Adp53547 Human 193 |
| 132 | 28 | 30.8 | 17 | 9 | AEB45051 | Aeb45051 B. bovis |
| 133 | 28 | 30.8 | 19 | 4 | ABB43798 | Abb43798 Peptide # |
| 134 | 28 | 30.8 | 19 | 4 | AAM77527 | Aam77527 Human bon |

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| 135 | 28 | 30.8 | 19 | 4 | AAM64763 | Aam64763 Human bra |
| 136 | 28 | 30.8 | 19 | 4 | ABG59171 | Abg59171 Human liv |
| 137 | 28 | 30.8 | 20 | 2 | AAR39832 | Aar39832 E1 peptid |
| 138 | 28 | 30.8 | 23 | 2 | AAR39881 | Aar39881 Lipopepti |
| 139 | 28 | 30.8 | 23 | 9 | AEE02004 | Aee02004 TM6 domai |
| 140 | 28 | 30.8 | 23 | 10 | AEF20557 | Aef20557 Human ost |
| 141 | 28 | 30.8 | 25 | 8 | ABO57373 | Abo57373 Human gen |
| 142 | 28 | 30.8 | 26 | 4 | AAB50221 | Aab50221 Membrane |
| 143 | 28 | 30.8 | 26 | 4 | AAB50202 | Aab50202 Membrane |
| 144 | 28 | 30.8 | 26 | 4 | AAB50204 | Aab50204 Membrane |
| 145 | 28 | 30.8 | 26 | 4 | AAB50219 | Aab50219 Membrane |
| 146 | 28 | 30.8 | 26 | 4 | AAB50201 | Aab50201 Membrane |
| 147 | 28 | 30.8 | 26 | 4 | AAB50210 | Aab50210 Membrane |
| 148 | 28 | 30.8 | 26 | 4 | AAB50217 | Aab50217 Membrane |
| 149 | 28 | 30.8 | 26 | 4 | AAB50228 | Aab50228 Membrane |
| 150 | 28 | 30.8 | 26 | 4 | AAB50229 | Aab50229 Membrane |
| 151 | 28 | 30.8 | 26 | 8 | ADH51590 | Adh51590 Bee venom |
| 152 | 28 | 30.8 | 26 | 8 | ADP87497 | Adp87497 Antimicro |
| 153 | 28 | 30.8 | 26 | 8 | ADR69294 | Adr69294 Apis flor |
| 154 | 28 | 30.8 | 27 | 4 | AAM18092 | Aam18092 Peptide # |
| 155 | 28 | 30.8 | 27 | 4 | AAB50213 | Aab50213 Membrane |
| 156 | 28 | 30.8 | 27 | 4 | AAB50216 | Aab50216 Membrane |
| 157 | 28 | 30.8 | 27 | 4 | AAB50227 | Aab50227 Membrane |
| 158 | 28 | 30.8 | 27 | 4 | AAB50223 | Aab50223 Membrane |
| 159 | 28 | 30.8 | 27 | 4 | AAB50214 | Aab50214 Membrane |
| 160 | 28 | 30.8 | 27 | 4 | AAB50225 | Aab50225 Membrane |
| 161 | 28 | 30.8 | 27 | 4 | ABB37128 | Abb37128 Peptide # |
| 162 | 28 | 30.8 | 27 | 4 | ABB31889 | Abb31889 Peptide # |
| 163 | 28 | 30.8 | 27 | 4 | ABB22439 | Abb22439 Protein # |
| 164 | 28 | 30.8 | 27 | 4 | AAM70265 | Aam70265 Human bon |
| 165 | 28 | 30.8 | 27 | 4 | AAM57847 | Aam57847 Human bra |
| 166 | 28 | 30.8 | 27 | 4 | ABG51963 | Abg51963 Human liv |
| 167 | 28 | 30.8 | 27 | 4 | AAM05727 | Aam05727 Peptide # |
| 168 | 28 | 30.8 | 27 | 5 | ABG39908 | Abg39908 Human pep |
| 169 | 28 | 30.8 | 27 | 5 | AAU90989 | Aau90989 Transplan |
| 170 | 28 | 30.8 | 27 | 9 | ADX08367 | Adx08367 Melittin |
| 171 | 28 | 30.8 | 28 | 2 | AAR89928 | Aar89928 A. cellul |
| 172 | 28 | 30.8 | 28 | 4 | AAB50218 | Aab50218 Membrane |
| 173 | 28 | 30.8 | 28 | 4 | AAB50230 | Aab50230 Membrane |
| 174 | 28 | 30.8 | 28 | 8 | ADH76878 | Adh76878 HGG-M2A p |
| 175 | 28 | 30.8 | 28 | 9 | ADV91068 | Adv91068 Human sod |
| 176 | 28 | 30.8 | 28 | 9 | ADV91067 | Adv91067 Human sod |
| 177 | 28 | 30.8 | 28 | 9 | ADV91069 | Adv91069 Human sod |
| 178 | 28 | 30.8 | 28 | 9 | ADX69186 | Adx69186 Voltage-g |
| 179 | 28 | 30.8 | 28 | 9 | ADX69187 | Adx69187 Voltage-g |
| 180 | 28 | 30.8 | 28 | 9 | ADX69188 | Adx69188 Voltage-g |
| 181 | 28 | 30.8 | 29 | 3 | AAB44873 | Aab44873 Human sec |
| 182 | 28 | 30.8 | 29 | 9 | AEB54587 | Aeb54587 Mouse pre |
| 183 | 28 | 30.8 | 30 | 1 | AAP98449 | Aap98449 Sequence |
| 184 | 28 | 30.8 | 30 | 2 | AAR74252 | Aar74252 Chlamydia |
| 185 | 28 | 30.8 | 30 | 2 | AAR91524 | Aar91524 Chlamydia |
| 186 | 28 | 30.8 | 30 | 5 | ABG68798 | Abg68798 C. tracho |
| 187 | 27.5 | 30.2 | 23 | 4 | AAM21121 | Aam21121 Peptide # |
| 188 | 27.5 | 30.2 | 23 | 4 | ABB43437 | Abb43437 Peptide # |
| 189 | 27.5 | 30.2 | 23 | 4 | AAM37325 | Aam37325 Peptide # |
| 190 | 27.5 | 30.2 | 23 | 4 | ABB26407 | Abb26407 Protein # |
| 191 | 27.5 | 30.2 | 23 | 4 | AAM64366 | Aam64366 Human bra |
| 192 | 27.5 | 30.2 | 23 | 4 | ABG58814 | Abg58814 Human liv |
| 193 | 27 | 29.7 | 10 | 6 | ABR05417 | Abr05417 Human can |
| 194 | 27 | 29.7 | 10 | 8 | ADS87097 | Ads87097 Human gen |
| 195 | 27 | 29.7 | 12 | 8 | ADP87492 | Adp87492 Antimicro |

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| 196 | 27 | 29.7 | 12 | 8 | AEB44138 | Aeb44138 Biomedica |
| 197 | 27 | 29.7 | 14 | 2 | AAW53471 | Aaw53471 P2 predom |
| 198 | 27 | 29.7 | 14 | 8 | ADG71721 | Adg71721 Human HGP |
| 199 | 27 | 29.7 | 15 | 2 | AAR89150 | Aar89150 CAEV env |
| 200 | 27 | 29.7 | 15 | 5 | AAU10987 | Aau10987 Human cel |
| 201 | 27 | 29.7 | 15 | 5 | ABG73581 | Abg73581 Human zin |
| 202 | 27 | 29.7 | 15 | 6 | ABR32470 | Abr32470 Human can |
| 203 | 27 | 29.7 | 15 | 6 | ABR32545 | Abr32545 Human can |
| 204 | 27 | 29.7 | 15 | 6 | ABR32424 | Abr32424 Human can |
| 205 | 27 | 29.7 | 15 | 6 | ABR31624 | Abr31624 Human can |
| 206 | 27 | 29.7 | 15 | 6 | ABR30390 | Abr30390 Human can |
| 207 | 27 | 29.7 | 15 | 6 | ABR30904 | Abr30904 Human can |
| 208 | 27 | 29.7 | 15 | 6 | ABR31077 | Abr31077 Human can |
| 209 | 27 | 29.7 | 15 | 6 | ABR32330 | Abr32330 Human can |
| 210 | 27 | 29.7 | 15 | 7 | ADE01056 | Ade01056 Human 193 |
| 211 | 27 | 29.7 | 15 | 7 | ADE00824 | Ade00824 Human 193 |
| 212 | 27 | 29.7 | 15 | 7 | ADE00975 | Ade00975 Human 193 |
| 213 | 27 | 29.7 | 15 | 7 | ADE00937 | Ade00937 Human 193 |
| 214 | 27 | 29.7 | 15 | 7 | ADE00728 | Ade00728 Human 193 |
| 215 | 27 | 29.7 | 15 | 7 | ADJ05378 | Adj05378 238P1B2 g |
| 216 | 27 | 29.7 | 15 | 7 | ADJ06118 | Adj06118 238P1B2 g |
| 217 | 27 | 29.7 | 15 | 7 | ADJ05727 | Adj05727 238P1B2 g |
| 218 | 27 | 29.7 | 15 | 7 | ADJ05820 | Adj05820 238P1B2 g |
| 219 | 27 | 29.7 | 15 | 7 | ADJ05460 | Adj05460 238P1B2 g |
| 220 | 27 | 29.7 | 15 | 7 | ADJ05775 | Adj05775 238P1B2 g |
| 221 | 27 | 29.7 | 15 | 7 | ADJ06061 | Adj06061 238P1B2 g |
| 222 | 27 | 29.7 | 15 | 7 | ADJ05908 | Adj05908 238P1B2 g |
| 223 | 27 | 29.7 | 15 | 7 | ADJ05404 | Adj05404 238P1B2 g |
| 224 | 27 | 29.7 | 15 | 7 | ADJ05620 | Adj05620 238P1B2 g |
| 225 | 27 | 29.7 | 15 | 7 | ADJ05867 | Adj05867 238P1B2 g |
| 226 | 27 | 29.7 | 15 | 7 | ADJ05377 | Adj05377 238P1B2 g |
| 227 | 27 | 29.7 | 15 | 7 | ADJ05621 | Adj05621 238P1B2 g |
| 228 | 27 | 29.7 | 15 | 7 | ADJ06215 | Adj06215 238P1B2 g |
| 229 | 27 | 29.7 | 15 | 7 | ADJ05967 | Adj05967 238P1B2 g |
| 230 | 27 | 29.7 | 15 | 7 | ADJ06183 | Adj06183 238P1B2 g |
| 231 | 27 | 29.7 | 15 | 8 | ADN58212 | Adn58212 238P1B2 H |
| 232 | 27 | 29.7 | 15 | 8 | ADN58309 | Adn58309 238P1B2 H |
| 233 | 27 | 29.7 | 15 | 8 | ADN58061 | Adn58061 238P1B2 H |
| 234 | 27 | 29.7 | 15 | 8 | ADN57554 | Adn57554 238P1B2 H |
| 235 | 27 | 29.7 | 15 | 8 | ADN57914 | Adn57914 238P1B2 H |
| 236 | 27 | 29.7 | 15 | 8 | ADN57821 | Adn57821 238P1B2 H |
| 237 | 27 | 29.7 | 15 | 8 | ADN58277 | Adn58277 238P1B2 H |
| 238 | 27 | 29.7 | 15 | 8 | ADN57714 | Adn57714 238P1B2 H |
| 239 | 27 | 29.7 | 15 | 8 | ADN57961 | Adn57961 238P1B2 H |
| 240 | 27 | 29.7 | 15 | 8 | ADN57715 | Adn57715 238P1B2 H |
| 241 | 27 | 29.7 | 15 | 8 | ADN58002 | Adn58002 238P1B2 H |
| 242 | 27 | 29.7 | 15 | 8 | ADN57472 | Adn57472 238P1B2 H |
| 243 | 27 | 29.7 | 15 | 8 | ADN57498 | Adn57498 238P1B2 H |
| 244 | 27 | 29.7 | 15 | 8 | ADN57869 | Adn57869 238P1B2 H |
| 245 | 27 | 29.7 | 15 | 8 | ADN58155 | Adn58155 238P1B2 H |
| 246 | 27 | 29.7 | 15 | 8 | ADN57471 | Adn57471 238P1B2 H |
| 247 | 27 | 29.7 | 15 | 8 | ADP53621 | Adp53621 Human 193 |
| 248 | 27 | 29.7 | 15 | 8 | ADP53772 | Adp53772 Human 193 |
| 249 | 27 | 29.7 | 15 | 8 | ADP53853 | Adp53853 Human 193 |
| 250 | 27 | 29.7 | 15 | 8 | ADP53525 | Adp53525 Human 193 |
| 251 | 27 | 29.7 | 15 | 8 | ADP53734 | Adp53734 Human 193 |
| 252 | 27 | 29.7 | 15 | 9 | AEB87611 | Aeb87611 Brain iso |
| 253 | 27 | 29.7 | 16 | 8 | ADO36463 | Ado36463 Intracell |
| 254 | 27 | 29.7 | 17 | 4 | ABB38962 | Abb38962 Peptide # |
| 255 | 27 | 29.7 | 17 | 4 | AAM32446 | Aam32446 Peptide # |
| 256 | 27 | 29.7 | 17 | 4 | AAM72186 | Aam72186 Human bon |

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|---|---|---|---|---|---|---|
| 257 | 27 | 29.7 | 17 | 4 | AAM59613 | Aam59613 Human bra |
| 258 | 27 | 29.7 | 17 | 4 | ABG53872 | Abg53872 Human liv |
| 259 | 27 | 29.7 | 17 | 5 | ABG42000 | Abg42000 Human pep |
| 260 | 27 | 29.7 | 17 | 8 | ADT39045 | Adt39045 hSARS vir |
| 261 | 27 | 29.7 | 17 | 8 | ADS78465 | Ads78465 SARS viru |
| 262 | 27 | 29.7 | 17 | 8 | ADT36575 | Adt36575 hSARS vir |
| 263 | 27 | 29.7 | 17 | 8 | ABY00078 | Aby00078 SARS coro |
| 264 | 27 | 29.7 | 18 | 2 | AAW09486 | Aaw09486 Thrombopo |
| 265 | 27 | 29.7 | 18 | 2 | AAW36637 | Aaw36637 Thrombopo |
| 266 | 27 | 29.7 | 18 | 4 | AAU25856 | Aau25856 Human thr |
| 267 | 27 | 29.7 | 18 | 9 | ADV22869 | Adv22869 HCV H77 i |
| 268 | 27 | 29.7 | 19 | 7 | ADF14607 | Adf14607 Rheumatoi |
| 269 | 27 | 29.7 | 19 | 8 | ADT39130 | Adt39130 hSARS vir |
| 270 | 27 | 29.7 | 19 | 8 | ADS78550 | Ads78550 SARS viru |
| 271 | 27 | 29.7 | 19 | 8 | ADT36660 | Adt36660 hSARS vir |
| 272 | 27 | 29.7 | 19 | 8 | ABY00163 | Aby00163 SARS coro |
| 273 | 27 | 29.7 | 19 | 8 | ABY03338 | Aby03338 SARS coro |
| 274 | 27 | 29.7 | 19 | 9 | AEC95996 | Aec95996 F. hetero |
| 275 | 27 | 29.7 | 20 | 2 | AAR55359 | Aar55359 Conformat |
| 276 | 27 | 29.7 | 20 | 2 | AAY01468 | Aay01468 Polypepti |
| 277 | 27 | 29.7 | 20 | 7 | ABO23439 | Abo23439 Amino aci |
| 278 | 27 | 29.7 | 20 | 8 | ADR20827 | Adr20827 Human sec |
| 279 | 27 | 29.7 | 21 | 2 | AAR72296 | Aar72296 Glutamic |
| 280 | 27 | 29.7 | 21 | 2 | AAW34051 | Aaw34051 Human MDR |
| 281 | 27 | 29.7 | 21 | 3 | AAY59588 | Aay59588 GAD65 fra |
| 282 | 27 | 29.7 | 21 | 8 | ADY81194 | Ady81194 Rice gene |
| 283 | 27 | 29.7 | 22 | 6 | ABP99586 | Abp99586 Human sec |
| 284 | 27 | 29.7 | 22 | 6 | ABR01068 | Abr01068 Human gen |
| 285 | 27 | 29.7 | 23 | 4 | AAM88237 | Aam88237 Human imm |
| 286 | 27 | 29.7 | 23 | 4 | AAB64425 | Aab64425 Human sec |
| 287 | 27 | 29.7 | 24 | 2 | AAW23485 | Aaw23485 Antibacte |
| 288 | 27 | 29.7 | 24 | 4 | AAU04309 | Aau04309 ATP-bindi |
| 289 | 27 | 29.7 | 25 | 2 | AAW03632 | Aaw03632 G-protein |
| 290 | 27 | 29.7 | 25 | 2 | AAY39442 | Aay39442 Human Bur |
| 291 | 27 | 29.7 | 25 | 2 | AAW90171 | Aaw90171 Triabin/t |
| 292 | 27 | 29.7 | 25 | 2 | AAW90170 | Aaw90170 Triabin/t |
| 293 | 27 | 29.7 | 25 | 5 | ABB82365 | Abb82365 M11L prot |
| 294 | 27 | 29.7 | 25 | 5 | AAO21800 | Aao21800 Lung-spec |
| 295 | 27 | 29.7 | 25 | 5 | AAU78042 | Aau78042 Human Bur |
| 296 | 27 | 29.7 | 25 | 6 | ABJ19229 | Abj19229 T helper |
| 297 | 27 | 29.7 | 25 | 9 | ADV26014 | Adv26014 Myxoma vi |
| 298 | 27 | 29.7 | 26 | 2 | AAR38837 | Aar38837 Melittin |
| 299 | 27 | 29.7 | 26 | 2 | AAR38838 | Aar38838 Melittin |
| 300 | 27 | 29.7 | 26 | 2 | AAY30916 | Aay30916 Human sec |
| 301 | 27 | 29.7 | 26 | 8 | ADG71689 | Adg71689 Human HGP |
| 302 | 27 | 29.7 | 26 | 10 | AEE37498 | Aee37498 Human ser |
| 303 | 27 | 29.7 | 27 | 8 | ADK50716 | Adk50716 Human car |
| 304 | 27 | 29.7 | 28 | 3 | AAB28711 | Aab28711 Human sec |
| 305 | 27 | 29.7 | 28 | 5 | ABG78096 | Abg78096 ITALY, LO |
| 306 | 27 | 29.7 | 28 | 8 | ADR45672 | Adr45672 Rat G pro |
| 307 | 27 | 29.7 | 28 | 9 | ADV91050 | Adv91050 Rat sodiu |
| 308 | 27 | 29.7 | 28 | 9 | ADV91043 | Adv91043 Human sod |
| 309 | 27 | 29.7 | 28 | 9 | ADV91049 | Adv91049 Rat sodiu |
| 310 | 27 | 29.7 | 28 | 9 | ADV91044 | Adv91044 Human sod |
| 311 | 27 | 29.7 | 28 | 9 | ADV91047 | Adv91047 Rat sodiu |
| 312 | 27 | 29.7 | 28 | 9 | ADX69166 | Adx69166 Voltage-g |
| 313 | 27 | 29.7 | 28 | 9 | ADX69168 | Adx69168 Voltage-g |
| 314 | 27 | 29.7 | 28 | 9 | ADX69169 | Adx69169 Voltage-g |
| 315 | 27 | 29.7 | 28 | 9 | ADX69162 | Adx69162 Voltage-g |
| 316 | 27 | 29.7 | 28 | 9 | ADX69163 | Adx69163 Voltage-g |
| 317 | 27 | 29.7 | 29 | 4 | AAB60729 | Aab60729 Human sec |

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|---|---|---|---|---|---|---|
| 318 | 27 | 29.7 | 29 | 5 | AAU98712 | Aau98712 Human cyc |
| 319 | 27 | 29.7 | 29 | 8 | ADP87495 | Adp87495 Antimicro |
| 320 | 27 | 29.7 | 29 | 8 | ADP87494 | Adp87494 Antimicro |
| 321 | 27 | 29.7 | 29 | 8 | AEB44140 | Aeb44140 Biomedica |
| 322 | 27 | 29.7 | 29 | 8 | AEB44141 | Aeb44141 Biomedica |
| 323 | 27 | 29.7 | 30 | 1 | AAP80653 | Aap80653 Peptide e |
| 324 | 27 | 29.7 | 30 | 2 | AAR05809 | Aar05809 Signal pe |
| 325 | 27 | 29.7 | 30 | 2 | AAY41529 | Aay41529 Fragment |
| 326 | 27 | 29.7 | 30 | 5 | AAU84648 | Aau84648 HCV HepC1 |
| 327 | 26.5 | 29.1 | 16 | 9 | AEA27278 | Aea27278 Stress to |
| 328 | 26.5 | 29.1 | 19 | 5 | AAU99839 | Aau99839 Human cat |
| 329 | 26.5 | 29.1 | 25 | 2 | AAR39772 | Aar39772 Melittin |
| 330 | 26.5 | 29.1 | 25 | 2 | AAR39770 | Aar39770 Melittin |
| 331 | 26.5 | 29.1 | 28 | 2 | AAW40014 | Aaw40014 Peptide e |
| 332 | 26.5 | 29.1 | 30 | 5 | ABP29172 | Abp29172 Streptoco |
| 333 | 26 | 28.6 | 9 | 2 | AAR51596 | Aar51596 Mimotope |
| 334 | 26 | 28.6 | 9 | 2 | AAR69971 | Aar69971 Nonameric |
| 335 | 26 | 28.6 | 9 | 2 | AAR98719 | Aar98719 Peptide 2 |
| 336 | 26 | 28.6 | 9 | 2 | AAY46520 | Aay46520 Immunogen |
| 337 | 26 | 28.6 | 9 | 7 | ADW32181 | Adw32181 HLA bindi |
| 338 | 26 | 28.6 | 9 | 7 | ADW31315 | Adw31315 HLA bindi |
| 339 | 26 | 28.6 | 10 | 9 | ADZ04488 | Adz04488 Alpha1-an |
| 340 | 26 | 28.6 | 12 | 6 | ABR42901 | Abr42901 Bovine hi |
| 341 | 26 | 28.6 | 12 | 9 | AEB94175 | Aeb94175 Serum CD2 |
| 342 | 26 | 28.6 | 13 | 6 | ABR59542 | Abr59542 S. aureus |
| 343 | 26 | 28.6 | 13 | 9 | AEB94174 | Aeb94174 Serum CD2 |
| 344 | 26 | 28.6 | 13 | 9 | AED27713 | Aed27713 Tyrosyl-t |
| 345 | 26 | 28.6 | 14 | 2 | AAW40030 | Aaw40030 Cytoplasm |
| 346 | 26 | 28.6 | 14 | 4 | AAG99376 | Aag99376 Proteasom |
| 347 | 26 | 28.6 | 14 | 4 | AAE05991 | Aae05991 Peptide # |
| 348 | 26 | 28.6 | 14 | 7 | ADH89139 | Adh89139 E. avium |
| 349 | 26 | 28.6 | 15 | 2 | AAR13975 | Aar13975 [Leu14]Me |
| 350 | 26 | 28.6 | 15 | 2 | AAR61466 | Aar61466 [Leu-14] |
| 351 | 26 | 28.6 | 15 | 7 | ADD24084 | Add24084 Breast ca |
| 352 | 26 | 28.6 | 15 | 7 | ADD23632 | Add23632 Breast ca |
| 353 | 26 | 28.6 | 15 | 8 | ADL70918 | Adl70918 PTP1B pho |
| 354 | 26 | 28.6 | 15 | 8 | ADL70822 | Adl70822 PTP1B pho |
| 355 | 26 | 28.6 | 15 | 8 | ADL70917 | Adl70917 PTP1B pho |
| 356 | 26 | 28.6 | 15 | 8 | ADP26537 | Adp26537 Plasmodiu |
| 357 | 26 | 28.6 | 16 | 7 | ADM47482 | Adm47482 Bioactive |
| 358 | 26 | 28.6 | 16 | 8 | ADI41077 | Adi41077 Human HGP |
| 359 | 26 | 28.6 | 16 | 8 | ADI41155 | Adi41155 Human HGP |
| 360 | 26 | 28.6 | 16 | 8 | ADI41115 | Adi41115 Human HGP |
| 361 | 26 | 28.6 | 17 | 7 | ADJ00164 | Adj00164 238P1B2 g |
| 362 | 26 | 28.6 | 17 | 8 | ADN52266 | Adn52266 238P1B2 H |
| 363 | 26 | 28.6 | 18 | 3 | AAB51856 | Aab51856 Human sec |
| 364 | 26 | 28.6 | 18 | 4 | AAG99373 | Aag99373 Proteasom |
| 365 | 26 | 28.6 | 18 | 7 | ADG73501 | Adg73501 Enterococ |
| 366 | 26 | 28.6 | 18 | 9 | AEC11101 | Aec11101 Enterococ |
| 367 | 26 | 28.6 | 18 | 10 | AEE36861 | Aee36861 Human ser |
| 368 | 26 | 28.6 | 19 | 2 | AAY16640 | Aay16640 WO9914235 |
| 369 | 26 | 28.6 | 19 | 3 | AAB28825 | Aab28825 Geminivir |
| 370 | 26 | 28.6 | 19 | 7 | ADJ00165 | Adj00165 238P1B2 g |
| 371 | 26 | 28.6 | 19 | 8 | ADH89725 | Adh89725 Cell pene |
| 372 | 26 | 28.6 | 19 | 8 | ADN52267 | Adn52267 238P1B2 H |
| 373 | 26 | 28.6 | 19 | 9 | ADX56727 | Adx56727 Cardiovas |
| 374 | 26 | 28.6 | 19 | 9 | ADY38118 | Ady38118 Human CPP |
| 375 | 26 | 28.6 | 19 | 9 | ADZ80725 | Adz80725 Amino aci |
| 376 | 26 | 28.6 | 19 | 9 | ADZ80726 | Adz80726 Amino aci |
| 377 | 26 | 28.6 | 19 | 9 | AED43095 | Aed43095 Persephin |
| 378 | 26 | 28.6 | 19 | 9 | AED68502 | Aed68502 Membrane- |

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|---|---|---|---|---|---|---|
| 379 | 26 | 28.6 | 19 | 9 | AED89965 | Aed89965 Membrane |
| 380 | 26 | 28.6 | 19 | 10 | AEE25291 | Aee25291 Transport |
| 381 | 26 | 28.6 | 19 | 10 | AEF51810 | Aef51810 Transport |
| 382 | 26 | 28.6 | 20 | 2 | AAR42715 | Aar42715 Guinea pi |
| 383 | 26 | 28.6 | 20 | 2 | AAR42714 | Aar42714 Murine TG |
| 384 | 26 | 28.6 | 20 | 2 | AAY40856 | Aay40856 Amino aci |
| 385 | 26 | 28.6 | 20 | 7 | ADF28112 | Adf28112 Complemen |
| 386 | 26 | 28.6 | 20 | 7 | ADF28102 | Adf28102 Complemen |
| 387 | 26 | 28.6 | 20 | 8 | ADH37342 | Adh37342 Epstein B |
| 388 | 26 | 28.6 | 20 | 8 | ADH37343 | Adh37343 Epstein B |
| 389 | 26 | 28.6 | 20 | 8 | ADU17214 | Adu17214 M. tuberc |
| 390 | 26 | 28.6 | 20 | 9 | ADW52238 | Adw52238 Human PL |
| 391 | 26 | 28.6 | 20 | 9 | ADZ98147 | Adz98147 Human ami |
| 392 | 26 | 28.6 | 20 | 9 | AEE34822 | Aee34822 Wheat gli |
| 393 | 26 | 28.6 | 20 | 9 | AEE34823 | Aee34823 Wheat gli |
| 394 | 26 | 28.6 | 20 | 10 | AEF09682 | Aef09682 Monkeypox |
| 395 | 26 | 28.6 | 21 | 2 | AAW34062 | Aaw34062 GPCR anta |
| 396 | 26 | 28.6 | 21 | 2 | AAW26292 | Aaw26292 Peptide 6 |
| 397 | 26 | 28.6 | 21 | 2 | AAW40031 | Aaw40031 Peptide d |
| 398 | 26 | 28.6 | 21 | 7 | ADJ93115 | Adj93115 Human G-c |
| 399 | 26 | 28.6 | 21 | 9 | ADY63840 | Ady63840 Human apo |
| 400 | 26 | 28.6 | 22 | 2 | AAR70673 | Aar70673 Transmemb |
| 401 | 26 | 28.6 | 22 | 7 | ADJ93201 | Adj93201 Human G-c |
| 402 | 26 | 28.6 | 22 | 9 | AED68501 | Aed68501 Membrane- |
| 403 | 26 | 28.6 | 22 | 9 | AED89964 | Aed89964 Membrane |
| 404 | 26 | 28.6 | 22 | 10 | AEE25290 | Aee25290 Transport |
| 405 | 26 | 28.6 | 22 | 10 | AEF51809 | Aef51809 Transport |
| 406 | 26 | 28.6 | 24 | 2 | AAR66208 | Aar66208 N-termina |
| 407 | 26 | 28.6 | 24 | 2 | AAW26284 | Aaw26284 Peptide A |
| 408 | 26 | 28.6 | 24 | 2 | AAW26285 | Aaw26285 Peptide A |
| 409 | 26 | 28.6 | 25 | 2 | AAR39760 | Aar39760 Melittin |
| 410 | 26 | 28.6 | 25 | 2 | AAR39765 | Aar39765 Melittin |
| 411 | 26 | 28.6 | 25 | 2 | AAR39763 | Aar39763 Melittin |
| 412 | 26 | 28.6 | 25 | 2 | AAR39761 | Aar39761 Melittin |
| 413 | 26 | 28.6 | 25 | 2 | AAR39766 | Aar39766 Melittin |
| 414 | 26 | 28.6 | 25 | 2 | AAR39768 | Aar39768 Melittin |
| 415 | 26 | 28.6 | 25 | 2 | AAR39762 | Aar39762 Melittin |
| 416 | 26 | 28.6 | 25 | 2 | AAR39769 | Aar39769 Melittin |
| 417 | 26 | 28.6 | 25 | 2 | AAR39783 | Aar39783 Melittin |
| 418 | 26 | 28.6 | 25 | 2 | AAR39764 | Aar39764 Melittin |
| 419 | 26 | 28.6 | 25 | 2 | AAR39782 | Aar39782 Melittin |
| 420 | 26 | 28.6 | 25 | 2 | AAR39767 | Aar39767 Melittin |
| 421 | 26 | 28.6 | 25 | 2 | AAM48358 | Aam48358 Antifunga |
| 422 | 26 | 28.6 | 25 | 3 | AAY71483 | Aay71483 Ehrlichia |
| 423 | 26 | 28.6 | 25 | 5 | AAU96113 | Aau96113 Ehrlichia |
| 424 | 26 | 28.6 | 25 | 7 | ADM80761 | Adm80761 Melittin |
| 425 | 26 | 28.6 | 25 | 8 | ADH89721 | Adh89721 Cell pene |
| 426 | 26 | 28.6 | 25 | 9 | AED68499 | Aed68499 Membrane- |
| 427 | 26 | 28.6 | 25 | 9 | AED89962 | Aed89962 Membrane |
| 428 | 26 | 28.6 | 25 | 10 | AEE25288 | Aee25288 Transport |
| 429 | 26 | 28.6 | 25 | 10 | AEF51807 | Aef51807 Transport |
| 430 | 26 | 28.6 | 26 | 1 | AAP91340 | Aap91340 Amino aci |
| 431 | 26 | 28.6 | 26 | 2 | AAR13908 | Aar13908 Guanidina |
| 432 | 26 | 28.6 | 26 | 2 | AAR22990 | Aar22990 Melittin |
| 433 | 26 | 28.6 | 26 | 2 | AAR39788 | Aar39788 Melittin |
| 434 | 26 | 28.6 | 26 | 2 | AAR38828 | Aar38828 Melittin |
| 435 | 26 | 28.6 | 26 | 2 | AAR39789 | Aar39789 Melittin |
| 436 | 26 | 28.6 | 26 | 2 | AAR39759 | Aar39759 Melittin |
| 437 | 26 | 28.6 | 26 | 2 | AAR38839 | Aar38839 Melittin |
| 438 | 26 | 28.6 | 26 | 2 | AAR38834 | Aar38834 Melittin |
| 439 | 26 | 28.6 | 26 | 2 | AAR39784 | Aar39784 Melittin |

| | | | | | | |
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| 440 | 26 | 28.6 | 26 | 2 | AAR39785 | Aar39785 Melittin |
| 441 | 26 | 28.6 | 26 | 2 | AAR38827 | Aar38827 Melittin |
| 442 | 26 | 28.6 | 26 | 2 | AAR39790 | Aar39790 Melittin |
| 443 | 26 | 28.6 | 26 | 2 | AAR35383 | Aar35383 Melittin |
| 444 | 26 | 28.6 | 26 | 2 | AAR45114 | Aar45114 Melittin |
| 445 | 26 | 28.6 | 26 | 2 | AAR50565 | Aar50565 Amphiphil |
| 446 | 26 | 28.6 | 26 | 2 | AAR55989 | Aar55989 Ion chann |
| 447 | 26 | 28.6 | 26 | 2 | AAR59067 | Aar59067 Melittin, |
| 448 | 26 | 28.6 | 26 | 2 | AAR56950 | Aar56950 Peptide w |
| 449 | 26 | 28.6 | 26 | 2 | AAR50430 | Aar50430 Amphiphil |
| 450 | 26 | 28.6 | 26 | 2 | AAR85516 | Aar85516 Melittin. |
| 451 | 26 | 28.6 | 26 | 2 | AAR72973 | Aar72973 Calmoduli |
| 452 | 26 | 28.6 | 26 | 2 | AAR90136 | Aar90136 Melittin |
| 453 | 26 | 28.6 | 26 | 2 | AAW08667 | Aaw08667 Honeybee |
| 454 | 26 | 28.6 | 26 | 2 | AAW09134 | Aaw09134 Melittin |
| 455 | 26 | 28.6 | 26 | 2 | AAW23502 | Aaw23502 Antibacte |
| 456 | 26 | 28.6 | 26 | 2 | AAW16374 | Aaw16374 Honeybee |
| 457 | 26 | 28.6 | 26 | 2 | AAW35146 | Aaw35146 Melittin- |
| 458 | 26 | 28.6 | 26 | 2 | AAW35145 | Aaw35145 Melittin- |
| 459 | 26 | 28.6 | 26 | 2 | AAW77385 | Aaw77385 Lytic pep |
| 460 | 26 | 28.6 | 26 | 2 | AAW66453 | Aaw66453 Cationic |
| 461 | 26 | 28.6 | 26 | 2 | AAW43128 | Aaw43128 Melittin, |
| 462 | 26 | 28.6 | 26 | 2 | AAW71674 | Aaw71674 Melittin- |
| 463 | 26 | 28.6 | 26 | 2 | AAW82879 | Aaw82879 Antipatho |
| 464 | 26 | 28.6 | 26 | 2 | AAW82880 | Aaw82880 Antipatho |
| 465 | 26 | 28.6 | 26 | 2 | AAY22019 | Aay22019 Melittin. |
| 466 | 26 | 28.6 | 26 | 2 | AAW87611 | Aaw87611 Antimicro |
| 467 | 26 | 28.6 | 26 | 2 | AAW95333 | Aaw95333 Synthetic |
| 468 | 26 | 28.6 | 26 | 2 | AAY10732 | Aay10732 Peptide u |
| 469 | 26 | 28.6 | 26 | 3 | AAB12439 | Aab12439 Plasmid c |
| 470 | 26 | 28.6 | 26 | 3 | AAY44325 | Aay44325 Antimicro |
| 471 | 26 | 28.6 | 26 | 3 | AAY91752 | Aay91752 Cationic |
| 472 | 26 | 28.6 | 26 | 3 | AAB17408 | Aab17408 Antipatho |
| 473 | 26 | 28.6 | 26 | 3 | AAB17407 | Aab17407 Antipatho |
| 474 | 26 | 28.6 | 26 | 3 | AAB17409 | Aab17409 Antipatho |
| 475 | 26 | 28.6 | 26 | 3 | AAB11034 | Aab11034 Apis mell |
| 476 | 26 | 28.6 | 26 | 4 | AAM20092 | Aam20092 Peptide # |
| 477 | 26 | 28.6 | 26 | 4 | AAB50205 | Aab50205 Membrane |
| 478 | 26 | 28.6 | 26 | 4 | AAB50209 | Aab50209 Membrane |
| 479 | 26 | 28.6 | 26 | 4 | AAB50199 | Aab50199 Membrane |
| 480 | 26 | 28.6 | 26 | 4 | AAB50200 | Aab50200 Membrane |
| 481 | 26 | 28.6 | 26 | 4 | AAB92169 | Aab92169 Signal tr |
| 482 | 26 | 28.6 | 26 | 4 | ABB40276 | Abb40276 Peptide # |
| 483 | 26 | 28.6 | 26 | 4 | ABB39475 | Abb39475 Peptide # |
| 484 | 26 | 28.6 | 26 | 4 | ABB42416 | Abb42416 Peptide # |
| 485 | 26 | 28.6 | 26 | 4 | AAM33959 | Aam33959 Peptide # |
| 486 | 26 | 28.6 | 26 | 4 | AAM36226 | Aam36226 Peptide # |
| 487 | 26 | 28.6 | 26 | 4 | AAM33012 | Aam33012 Peptide # |
| 488 | 26 | 28.6 | 26 | 4 | AAG99362 | Aag99362 Proteasom |
| 489 | 26 | 28.6 | 26 | 4 | AAB50842 | Aab50842 Bee prote |
| 490 | 26 | 28.6 | 26 | 4 | ABB25868 | Abb25868 Protein # |
| 491 | 26 | 28.6 | 26 | 4 | ABB24689 | Abb24689 Protein # |
| 492 | 26 | 28.6 | 26 | 4 | AAM73772 | Aam73772 Human bon |
| 493 | 26 | 28.6 | 26 | 4 | AAM72782 | Aam72782 Human bon |
| 494 | 26 | 28.6 | 26 | 4 | AAM76117 | Aam76117 Human bon |
| 495 | 26 | 28.6 | 26 | 4 | AAM63301 | Aam63301 Human bra |
| 496 | 26 | 28.6 | 26 | 4 | AAM61069 | Aam61069 Human bra |
| 497 | 26 | 28.6 | 26 | 4 | AAM60166 | Aam60166 Human bra |
| 498 | 26 | 28.6 | 26 | 4 | ABG57838 | Abg57838 Human liv |
| 499 | 26 | 28.6 | 26 | 4 | ABG55518 | Abg55518 Human liv |
| 500 | 26 | 28.6 | 26 | 4 | ABG54483 | Abg54483 Human liv |

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| 501 | 26 | 28.6 | 26 | 4 | AAY72458 | Aay72458 Mellitin |
| 502 | 26 | 28.6 | 26 | 5 | AAM49738 | Aam49738 Peptide f |
| 503 | 26 | 28.6 | 26 | 5 | ABG43657 | Abg43657 Human pep |
| 504 | 26 | 28.6 | 26 | 5 | ABG45484 | Abg45484 Human pep |
| 505 | 26 | 28.6 | 26 | 5 | ABG42607 | Abg42607 Human pep |
| 506 | 26 | 28.6 | 26 | 5 | ABB73012 | Abb73012 Antipatho |
| 507 | 26 | 28.6 | 26 | 5 | ABB73010 | Abb73010 Antipatho |
| 508 | 26 | 28.6 | 26 | 5 | ABB73011 | Abb73011 Antipatho |
| 509 | 26 | 28.6 | 26 | 5 | ABB81941 | Abb81941 Peptide f |
| 510 | 26 | 28.6 | 26 | 5 | AAE18196 | Aae18196 Apis mell |
| 511 | 26 | 28.6 | 26 | 5 | AAE18198 | Aae18198 Procytoto |
| 512 | 26 | 28.6 | 26 | 5 | AAE22445 | Aae22445 Biologica |
| 513 | 26 | 28.6 | 26 | 5 | ABB81263 | Abb81263 [D]-Melit |
| 514 | 26 | 28.6 | 26 | 5 | ABB81262 | Abb81262 Melittin |
| 515 | 26 | 28.6 | 26 | 5 | AAO21742 | Aao21742 Melittin |
| 516 | 26 | 28.6 | 26 | 5 | AAO21734 | Aao21734 Melittin |
| 517 | 26 | 28.6 | 26 | 5 | AAO21740 | Aao21740 Procytoto |
| 518 | 26 | 28.6 | 26 | 6 | ABU07618 | Abu07618 Crystal a |
| 519 | 26 | 28.6 | 26 | 6 | ABU59630 | Abu59630 Cationic |
| 520 | 26 | 28.6 | 26 | 6 | ABR00830 | Abr00830 Bioactive |
| 521 | 26 | 28.6 | 26 | 7 | ADF18363 | Adf18363 Antibacte |
| 522 | 26 | 28.6 | 26 | 7 | ADG88568 | Adg88568 Crystal a |
| 523 | 26 | 28.6 | 26 | 7 | ADJ73166 | Adj73166 Antipatho |
| 524 | 26 | 28.6 | 26 | 7 | ADJ73165 | Adj73165 Antipatho |
| 525 | 26 | 28.6 | 26 | 7 | ADJ73164 | Adj73164 Antipatho |
| 526 | 26 | 28.6 | 26 | 8 | ADJ52801 | Adj52801 CH1 delet |
| 527 | 26 | 28.6 | 26 | 8 | ADJ52800 | Adj52800 CH1 delet |
| 528 | 26 | 28.6 | 26 | 8 | ADJ52799 | Adj52799 CH1 delet |
| 529 | 26 | 28.6 | 26 | 8 | ADJ51762 | Adj51762 CH1 delet |
| 530 | 26 | 28.6 | 26 | 8 | ADJ51760 | Adj51760 CH1 delet |
| 531 | 26 | 28.6 | 26 | 8 | ADJ51761 | Adj51761 CH1 delet |
| 532 | 26 | 28.6 | 26 | 8 | ADJ78628 | Adj78628 Purificat |
| 533 | 26 | 28.6 | 26 | 8 | ADO59380 | Ado59380 Melittin |
| 534 | 26 | 28.6 | 26 | 8 | ADP74183 | Adp74183 Melittin |
| 535 | 26 | 28.6 | 26 | 8 | ADR12685 | Adr12685 Bee melit |
| 536 | 26 | 28.6 | 26 | 8 | ADU69235 | Adu69235 Honey bee |
| 537 | 26 | 28.6 | 26 | 9 | ADW73980 | Adw73980 Honey bee |
| 538 | 26 | 28.6 | 26 | 9 | ADY67501 | Ady67501 Tumor cel |
| 539 | 26 | 28.6 | 26 | 9 | ADZ60124 | Adz60124 Melittin |
| 540 | 26 | 28.6 | 26 | 9 | AEA47560 | Aea47560 Amino aci |
| 541 | 26 | 28.6 | 26 | 9 | AEC60349 | Aec60349 Biodegrad |
| 542 | 26 | 28.6 | 26 | 9 | AEC60348 | Aec60348 Biodegrad |
| 543 | 26 | 28.6 | 26 | 10 | AEE36724 | Aee36724 Human ser |
| 544 | 26 | 28.6 | 26 | 10 | AEE99045 | Aee99045 Tumor tis |
| 545 | 26 | 28.6 | 26 | 10 | AEF61738 | Aef61738 Modified |
| 546 | 26 | 28.6 | 26 | 10 | AEF61737 | Aef61737 Modified |
| 547 | 26 | 28.6 | 26 | 10 | AEF61736 | Aef61736 Modified |
| 548 | 26 | 28.6 | 26 | 10 | AEF69156 | Aef69156 ES-HER2/n |
| 549 | 26 | 28.6 | 26 | 10 | AEG07876 | Aeg07876 Peptide 2 |
| 550 | 26 | 28.6 | 27 | 2 | AAW66392 | Aaw66392 Bee venom |
| 551 | 26 | 28.6 | 27 | 5 | ABB81271 | Abb81271 Antibacte |
| 552 | 26 | 28.6 | 27 | 5 | ABB81236 | Abb81236 Antibacte |
| 553 | 26 | 28.6 | 27 | 8 | ABO56899 | Abo56899 Human gen |
| 554 | 26 | 28.6 | 27 | 8 | ADK49194 | Adk49194 Human car |
| 555 | 26 | 28.6 | 27 | 9 | ADV60176 | Adv60176 COX pepti |
| 556 | 26 | 28.6 | 27 | 9 | AEC32680 | Aec32680 Keratinoc |
| 557 | 26 | 28.6 | 28 | 1 | AAP60883 | Aap60883 Synthetic |
| 558 | 26 | 28.6 | 28 | 2 | AAY02954 | Aay02954 Fragment |
| 559 | 26 | 28.6 | 28 | 4 | AAM13591 | Aam13591 Peptide # |
| 560 | 26 | 28.6 | 28 | 4 | ABB32521 | Abb32521 Peptide # |
| 561 | 26 | 28.6 | 28 | 4 | AAM25989 | Aam25989 Peptide # |

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| 562 | 26 | 28.6 | 28 | 4 | AAB85397 | Aab85397 Stem cell |
| 563 | 26 | 28.6 | 28 | 4 | ABB27373 | Abb27373 Human pep |
| 564 | 26 | 28.6 | 28 | 4 | ABB18026 | Abb18026 Protein # |
| 565 | 26 | 28.6 | 28 | 4 | AAM65732 | Aam65732 Human bon |
| 566 | 26 | 28.6 | 28 | 4 | AAM53353 | Aam53353 Human bra |
| 567 | 26 | 28.6 | 28 | 4 | ABG47373 | Abg47373 Human liv |
| 568 | 26 | 28.6 | 28 | 4 | AAM01341 | Aam01341 Peptide # |
| 569 | 26 | 28.6 | 28 | 5 | ABG35361 | Abg35361 Human pep |
| 570 | 26 | 28.6 | 28 | 6 | ABO01431 | Abo01431 Human ste |
| 571 | 26 | 28.6 | 28 | 6 | ABR63692 | Abr63692 Human bre |
| 572 | 26 | 28.6 | 28 | 7 | ADA07789 | Ada07789 Human sec |
| 573 | 26 | 28.6 | 28 | 8 | ADN41475 | Adn41475 Novel hum |
| 574 | 26 | 28.6 | 28 | 9 | ADV91039 | Adv91039 Human sod |
| 575 | 26 | 28.6 | 28 | 9 | ADV91041 | Adv91041 Human sod |
| 576 | 26 | 28.6 | 28 | 9 | ADV91042 | Adv91042 Human sod |
| 577 | 26 | 28.6 | 28 | 9 | ADV91040 | Adv91040 Human sod |
| 578 | 26 | 28.6 | 28 | 9 | ADV91045 | Adv91045 Human sod |
| 579 | 26 | 28.6 | 28 | 9 | ADV91046 | Adv91046 Rat sodiu |
| 580 | 26 | 28.6 | 28 | 9 | ADX69165 | Adx69165 Voltage-g |
| 581 | 26 | 28.6 | 28 | 9 | ADX69158 | Adx69158 Voltage-g |
| 582 | 26 | 28.6 | 28 | 9 | ADX69160 | Adx69160 Voltage-g |
| 583 | 26 | 28.6 | 28 | 9 | ADX69159 | Adx69159 Voltage-g |
| 584 | 26 | 28.6 | 28 | 9 | ADX69164 | Adx69164 Voltage-g |
| 585 | 26 | 28.6 | 28 | 9 | ADX69161 | Adx69161 Voltage-g |
| 586 | 26 | 28.6 | 29 | 2 | AAR09355 | Aar09355 Sequence |
| 587 | 26 | 28.6 | 29 | 3 | AAY65201 | Aay65201 Human 5' |
| 588 | 26 | 28.6 | 29 | 7 | ADJ00166 | Adj00166 238P1B2 g |
| 589 | 26 | 28.6 | 29 | 8 | ADN52268 | Adn52268 238P1B2 H |
| 590 | 26 | 28.6 | 29 | 8 | ADU72765 | Adu72765 Signal pe |
| 591 | 26 | 28.6 | 29 | 9 | ADZ73756 | Adz73756 Human inc |
| 592 | 26 | 28.6 | 30 | 2 | AAR98027 | Aar98027 Fusogenic |
| 593 | 26 | 28.6 | 30 | 3 | AAY64891 | Aay64891 Human 5' |
| 594 | 26 | 28.6 | 30 | 4 | AAU30169 | Aau30169 Novel hum |
| 595 | 26 | 28.6 | 30 | 5 | AAU84956 | Aau84956 Human Trp |

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Sequence 209, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
;  APPLICANT: Kantor, Aaron B.
;  APPLICANT:  Schulman, Howard
;  APPLICANT:  Becker, Christopher
;  TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
;  FILE REFERENCE: SURR.121
;  CURRENT APPLICATION NUMBER: US/10/801,990
;  CURRENT FILING DATE:  2004-03-15
;  PRIOR APPLICATION NUMBER: US 60/455,037
;  PRIOR FILING DATE: 2003-03-14
;  NUMBER OF SEQ ID NOS: 395
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-801-990-209

  Query Match             33.0%;  Score 30;  DB 5;  Length 17;
  Best Local Similarity   85.7%;  Pred. No. 6.5e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FALVSYI 13
              ||||:||
Db          8 FALVNYI 14
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Sequence 10, Application US/09178093B
; Patent No. 6660846
; GENERAL INFORMATION:
;  APPLICANT: Robert H. Edwards
;  APPLICANT:  Richard J. Reimer
;  APPLICANT:  Steve L. McIntire
;  APPLICANT:  Erik M. Jorgenson
;  APPLICANT:  Kim Schuske
;  TITLE OF INVENTION: Vesicular Amino Acid Transported
;  TITLE OF INVENTION:  Composition and Method
;  FILE REFERENCE: 2002-0005.30
;  CURRENT APPLICATION NUMBER: US/09/178,093B
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: 60/063,012
;  PRIOR FILING DATE: 1997-10-23
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-178-093B-10

  Query Match             36.3%;  Score 33;  DB 2;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GTFALVSYI 13
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Db         11 GLFALVAYL 19
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Sequence 33, Application US/07643343A
; Patent No. 5235038
;  GENERAL INFORMATION:
;    APPLICANT:  Blondelle, Sylvie E.
;    APPLICANT:  Houghten, Richard A.
;    TITLE OF INVENTION:  Deletion and Substitution
;    TITLE OF INVENTION:  Analogues of Melittin Peptide
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi & Stewart
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  DW4.V2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/643,343A
;      FILING DATE:  19910122
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  421250-139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  substitution analogue of melittin
;      NAME/KEY:  peptide
US-07-643-343A-33

  Query Match             33.0%;  Score 30;  DB 1;  Length 26;
  Best Local Similarity   53.8%;  Pred. No. 1.8e+02;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 LGTFALVSYIANK 16
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Db         11 LGLPALISWIKRK 23
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Sequence 42, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
;  GENERAL INFORMATION:
;    APPLICANT:  Dower, William J.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Cwirla, Steven E.
;    APPLICANT:  Gates, Christian
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Balasubramanian, Palaniappan
;    APPLICANT:  Wagstrom, Christopher R.
;    APPLICANT:  Hendren, Richard W.
;    APPLICANT:  Deprince, Randolph B.
;    APPLICANT:  Podduturi, Surekha
;    APPLICANT:  Yin, Qun
;    TITLE OF INVENTION:  PEPTIDES AND COMPOUNDS THAT BIND TO A
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  244
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Glaxo Wellcome
;      STREET:  Five Moore Drive, P.O. Box 13398
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,640
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hrubiec, Robert T.
;      REGISTRATION NUMBER:  36,392
;      REFERENCE/DOCKET NUMBER:  PK3281
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-248-1000
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-764-640-42

  Query Match             29.7%;  Score 27;  DB 1;  Length 18;
  Best Local Similarity   62.5%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LGTFALVS 11
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Db         11 LGSFSLLS 18
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Sequence 42, Application US/09516704
; Patent No. 6251864
;   GENERAL INFORMATION:
;        APPLICANT: Dower, William J.
;                   Barrett, Ronald W.
;                   Cwirla, Steven E.
;                   Gates, Christian
;                   Schatz, Peter J.
;                   Balasubramanian, Palaniappan
;                   Wagstrom, Christopher R.
;                   Hendren, Richard W.
;                   Deprince, Randolph B.
;                   Podduturi, Surekha
;        TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;                            RECEPTOR
;        NUMBER OF SEQUENCES: 244
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Glaxo Wellcome
;             STREET: Five Moore Drive, P.O. Box 13398
;             CITY: Research Triangle Park
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 27709
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/516,704
;             FILING DATE: 01-Mar-2000
;             CLASSIFICATION:
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hrubiec, Robert T.
;             REGISTRATION NUMBER: 36,392
;             REFERENCE/DOCKET NUMBER: PK3281
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 919-248-1000
;   INFORMATION FOR SEQ ID NO: 42:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 amino acids
;             TYPE: amino acid
;             STRANDEDNESS:
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-516-704-42

  Query Match             29.7%;  Score 27;  DB 2;  Length 18;
  Best Local Similarity   62.5%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LGTFALVS 11
              ||:|:|:|
Db         11 LGSFSLLS 18
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AAY17917
ID   AAY17917 standard; peptide; 21 AA.
XX
AC   AAY17917;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Vesicle transporter protein, RUNC-47 transmembrane domain 6.
XX
KW   Vesicle transporter protein; synaptic vesicle; UNC-47; RUNC-47; GABA;
KW   central nervous system disorder; peripheral nervous system disorder;
KW   neuropsychiatric; neuronal deficiency; gamma-aminobutyric acid; sedative;
KW   anxiolytic; transmembrane domain.
XX
OS   Rattus sp.
XX
PN   WO9920645-A1.
XX
PD   29-APR-1999.
XX
PF   23-OCT-1998;   98WO-US022587.
XX
PR   23-OCT-1997;   97US-0063012P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Edwards RH,  Reimer RJ,  Mcintire SL,  Jorgenson EM,  Schuske K;
XX
DR   WPI; 1999-302716/25.
XX
PT   Vesicular transporter protein useful for treating disorders of the
PT   central and/or peripheral nervous system.
XX
PS   Claim 3; Fig 1A-B; 52pp; English.
XX
CC   The invention relates to an amino acid synaptic vesicle transporter
CC   protein, UNC-47 and its rat homolog, RUNC-47. The vesicle transporter
CC   proteins can be used to identify candidate compounds that modulate amino
CC   acid transport into synaptic vesicles, these may be useful for treating
CC   disorders of the central and/or peripheral nervous system. RUNC-47 can be
CC   used to treat a subject having a neuropsychiatric condition characterised
CC   by neuronal deficiency of GABA (gamma-aminobutyric acid). Modulators of
CC   the proteins may also be useful for enhancing GABA uptake, which may
CC   produce sedative or anxiolytic effects. Sequences AAY17912-921 represent
CC   the transmembrane domains of the rat vesicular GABA transporter, RUNC-47
XX
SQ   Sequence 21 AA;

  Query Match             36.3%;  Score 33;  DB 2;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GTFALVSYI 13
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Db         11 GLFALVAYL 19
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AAR61467
ID   AAR61467 standard; peptide; 15 AA.
XX
AC   AAR61467;
XX
DT   16-SEP-1995  (first entry)
XX
DE   [Phe- or D-Phe-14] melittin-(7-21) analogue.
XX
KW   Peptide solid phase synthesis; polystyrene-grafted substrate; melittin.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 8
FT                   /note= "Phe or D-Phe"
XX
PN   US5373053-A.
XX
PD   13-DEC-1994.
XX
PF   14-DEC-1992;   92US-00990584.
XX
PR   01-SEP-1988;   88US-00239525.
PR   25-AUG-1989;   89US-00398846.
PR   12-MAY-1992;   92US-00882059.
XX
PA   (RISO-) RISO NAT LAB.
XX
PI   Berg RH,  Holm A,  Tam JP,  Pedersen WB,  Merrifield RB,  Almdal K;
XX
DR   WPI; 1995-030351/04.
XX
PT   substrate grafted with polystyrene - used in peptide synthesis giving
PT   high yields.
XX
PS   Example 9; Fig 3; 20pp; English.
XX
CC   The invention relates to a solid phase peptide synthesis method using a
CC   support consisting of a functionalised polystyrene-grafted polymer
CC   substrate. The peptides are prepared in high yield and purity. The
CC   process may be used for compartmentalised synthesis of a number of
CC   different peptides in parallel. The present sequence is one of 13
CC   melittin-(7-21) analogues prepared in parallel by the process (AAR61460-
CC   R61470)
XX
SQ   Sequence 15 AA;

  Query Match             35.2%;  Score 32;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GTFALVSYI 13
              | |||:|:|
Db          6 GLFALISWI 14
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AAR13129
ID   AAR13129 standard; protein; 15 AA.
XX
AC   AAR13129;
XX
DT   25-MAR-2003  (revised)
DT   01-OCT-1991  (first entry)
XX
DE   GPIb alpha peptide fragment.
XX
KW   Von Willebrand factor; vWF; platelet membrane glycoprotein Ib;
KW   glycoalicin; thrombosis.
XX
OS   Synthetic.
XX
PN   WO9109614-A.
XX
PD   11-JUL-1991.
XX
PF   04-JAN-1990;   90US-00460674.
XX
PR   04-JAN-1990;   90US-00460674.
PR   14-NOV-1990;   90US-00613083.
XX
PA   (SCRI ) SCRIPPS CLINIC & RES FOUND.
XX
PI   Ruggeri ZM,  Zimmerman TS,  Houghten RA,  Vicente V,  Mohri H;
PI   Ware JL;
XX
DR   WPI; 1991-222654/30.
XX
PT   GPIb alpha peptide fragment - inhibits binding of von Willebrand factor
PT   to platelet membrane glyco-protein Ib, useful in treating thrombosis.
XX
PS   Claim 1; Page 56; 76pp; English.
XX
CC   The peptide corresponds to residues 71-85 of the N-terminus of
CC   glycoalicin, a water sol. proteolytic fragment of GPIb alpha. It may be
CC   linked to a second peptide from the 45 kD N-terminal tryptic fragment of
CC   GPIb alpha. The peptide inhibits binding of vWF to GPIb. It can be used
CC   to inhibit activation, aggregation and/or adhesion of platelets, esp. for
CC   inhibition of thrombosis. See also AAR13128-R13138. (Updated on 25-MAR-
CC   2003 to correct PA field.)
XX
SQ   Sequence 15 AA;

  Query Match             33.0%;  Score 30;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 IPVLGTFAL 9
              :|||||  |
Db          6 LPVLGTLDL 14
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ADS13418
ID   ADS13418 standard; peptide; 17 AA.
XX
AC   ADS13418;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human rheumatoid arthritis marker peptide - SEQ ID 209.
XX
KW   rheumatoid arthritis; marker; antiinflammtory; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO2004082617-A2.
XX
PD   30-SEP-2004.
XX
PF   15-MAR-2004; 2004WO-US007880.
XX
PR   14-MAR-2003; 2003US-0455037P.
XX
PA   (SURR-) SURROMED INC.
XX
PI   Kantor AB,  Becker CH,  Schulman H;
XX
DR   WPI; 2004-690929/67.
XX
PT   New isolated marker for rheumatoid arthritis, useful in preparing a
PT   composition for diagnosing or treating rheumatoid arthritis.
XX
PS   Claim 1; SEQ ID NO 209; 184pp; English.
XX
CC   The invention relates to a novel isolated marker for rheumatoid arthritis
CC   selected from one of many (around 400) markers defined in the
CC   specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC   the small joints which is estimated to affect 2.1 million people in the
CC   United States alone. Current approaches to treat the disease include the
CC   use of non-steroidal antiinflammtory drugs (NSAIDS), which may reduce
CC   pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC   drugs (DMARDS), which act to slow the progression of the disease and
CC   avoid further joint injury. These drugs are associated with a number of
CC   serious side effects and the search for improved therapeutics is a
CC   subject of active research. The marker of the invention demonstrates
CC   antiarthritic activity and may be useful in preparing a composition for
CC   diagnosing or treating rheumatoid arthritis. The current sequence is that
CC   of a human rheumatoid arthritis marker peptide of the invention.
XX
SQ   Sequence 17 AA;

  Query Match             33.0%;  Score 30;  DB 8;  Length 17;
  Best Local Similarity   85.7%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FALVSYI 13
              ||||:||
Db          8 FALVNYI 14
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